SEQUENCE LISTING

<110> INTREXON CORPORATION

<120> EXPRESSION OF NOVEL CELL TAGS

<130> 50471-708.601

<140>
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<150> 62/516,639
<151> 2017-06-07

<160> 240

<170> PatentIn version 3.5

<210> 1
<211> 66
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
GMCSFR alpha signal sequence

<400> 1
atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacacccagc attcctcctg 60

atccca 66

<210> 2
<211> 22
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
GMCSFR alpha signal sequence

<400> 2
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro
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<210> 3
<211> 60
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
Ig Kappa signal sequence

<400> 3
atgaggctcc ctgctcagct cctggggctg ctaatgctct gggtcccagg atccagtggg 60

<210> 4
<211> 20
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Ig Kappa signal sequence

<400> 4
Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1 5 10 15

Gly Ser Ser Gly
20

<210> 5
<211> 54
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
Immunoglobulin E signal sequence

<400> 5
atggattgga cctggattct gtttctggtg gccgctgcca caagagtgca cagc 54

<210> 6
<211> 18
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown:
Immunoglobulin E signal sequence

<400> 6
Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1 5 10 15

His Ser

<210> 7
<211> 63
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
CD8-alpha signal sequence

<400> 7
atggcgctgc ccgtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccg 63

<210> 8
<211> 21
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
CD8-alpha signal sequence

<400> 8
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 9

<211> 63
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
TVB2(T21A) signal sequence

<400> 9
atgggcacca gcctcctctg ctggatggcc ctgtgtctcc tgggggcaga tcacgcagat 60

gct 63

<210> 10
<211> 21
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
TVB2(T21A) signal sequence

<400> 10
Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Ala
20

<210> 11
<211> 72
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
CD52 signal sequence

<400> 11
atgaagcgct tcctcttcct cctactcacc atcagcctcc tggttatggt acagatacaa 60

actggactct ca 72

<210> 12
<211> 24

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
CD52 signal sequence

<400> 12
Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser
20

<210> 13
<211> 84
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
Low-affinity nerve growth factor receptor
(LNGFR, TNFRSF16) signal sequence

<400> 13
atgggggcag gtgccaccgg ccgcgccatg gacgggccgc gcctgctgct gttgctgctt 60

ctgggggtgt cccttggagg tgcc 84

<210> 14
<211> 28
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Low-affinity nerve growth factor receptor
(LNGFR, TNFRSF16) signal sequence

<400> 14
Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
1 5 10 15

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala
20 25

<210> 15
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15
ggaagcgga 9

<210> 16
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 16
Gly Ser Gly
1

<210> 17
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 17
agtggcagcg gc 12

<210> 18
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

peptide

<400> 18
Ser Gly Ser Gly
1

<210> 19
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 19
ggcggaggcg gaagcggagg cggaggctcc ggcggaggcg gaagc 45

<210> 20
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 20
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 21
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 21
ggtggcggtg gctcgggcgg tggtgggtcg ggtggcggcg gatctggtgg cggtggctcg 60

<210> 22
<211> 20

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 22
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 23
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 23
ggcagcacct ccggcagcgg caagcctggc agcggcgagg gcagcaccaa gggc 54

<210> 24
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 24
Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
1 5 10 15

Lys Gly

<210> 25
<211> 78

<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
Glycophorin A (E91-R116) sequence

<400> 25
gagataacac tcattatttt tggggtgatg gctggtgtta ttggaacgat cctcttaatt 60

tcttacggta ttcgccga 78

<210> 26
<211> 26
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Glycophorin A (E91-R116) sequence

<400> 26
Glu Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr
1 5 10 15

Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg
20 25

<210> 27
<211> 69
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
Glycophorin A (I92-I114) sequence

<400> 27
ataacactca ttatttttgg ggtgatggct ggtgttattg gaacgatcct cttaatttct 60

tacggtatt 69

<210> 28
<211> 23
<212> PRT

<213> Unknown

<220>
<223> Description of Unknown:
Glycophorin A (I92-I114) sequence

<400> 28
Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile
1 5 10 15

Leu Leu Ile Ser Tyr Gly Ile
20

<210> 29
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 29
ataacactca ttatttttgg ggtgatggct ggtgttattg gaacgatcct cttagccctg 60

ctcatctgg 69

<210> 30
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 30
Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile
1 5 10 15

Leu Leu Ala Leu Leu Ile Trp
20

<210> 31

<211> 63
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
CD3 zeta (CD247) transmembrane domain sequence

<400> 31
ctctgctacc tgctggatgg aatcctcttc atctatggtg tcattctcac tgccttgttc 60

ctg 63

<210> 32
<211> 21
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
CD3 zeta (CD247) transmembrane domain sequence

<400> 32
Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu
1 5 10 15

Thr Ala Leu Phe Leu
20

<210> 33
<211> 84
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
CD8-alpha transmembrane domain sequence

<400> 33
atctacatct gggcccctct ggccggcacc tgtggcgtgc tgctgctgag cctggtcatc 60

accctgtact gcaaccaccg gaat 84

<210> 34
<211> 28

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
CD8-alpha transmembrane domain sequence

<400> 34
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
20 25

<210> 35
<211> 81
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
CD28 transmembrane domain sequence

<400> 35
ttttgggtgc tggtggtggt tggtggagtc ctggcttgct atagcttgct agtaacagtg 60

gcctttatta ttttctgggt g 81

<210> 36
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
CD28 transmembrane domain sequence

<400> 36
Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 37
<211> 63
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
Cytotoxic T-lymphocyte protein 4 transmembrane domain sequence

<400> 37
ttcctcctct ggatccttgc agcagttagt tcggggttgt ttttttatag ctttctcctc 60

aca 63

<210> 38
<211> 21
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Cytotoxic T-lymphocyte protein 4 transmembrane domain sequence

<400> 38
Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr
1 5 10 15

Ser Phe Leu Leu Thr
20

<210> 39
<211> 66
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
Low-affinity nerve growth factor receptor
(LNGFR, TNFRSF16) transmembrane domain sequence

<400> 39
ctcatccctg tctattgctc catcctggct gctgtggttg tgggccttgt ggcctacata 60

gccttc 66

<210> 40
<211> 22
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Low-affinity nerve growth factor receptor
(LNGFR, TNFRSF16) transmembrane domain sequence

<400> 40
Leu Ile Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu
1 5 10 15

Val Ala Tyr Ile Ala Phe
20

<210> 41
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 41
gcaacgaact tctctctcct aaaacaggct ggtgatgtgg aggagaatcc tggtcca 57

<210> 42
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 42
Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 43
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 43
cagtgtacta attatgctct cttgaaattg gctggagatg ttgagagcaa ccctggacct 60

<210> 44
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 44
Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
20

<210> 45
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 45
gagggcagag gaagtctgct aacatgcggt gacgtcgagg agaatcctgg acct 54

<210> 46
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 46
Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

<210> 47
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 47
gtcaaacaga ccctaaactt tgatctgcta aaactggccg gggatgtgga aagtaatccc 60

ggcccc 66

<210> 48
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 48
Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
20

<210> 49
<211> 570

<212> DNA
<213> Encephalomyocarditis virus

<400> 49
ccccctctcc ctcccccccc cctaacgtta ctggccgaag ccgcttggaa taaggccggt 60

gtgcgtttgt ctatatgtta ttttccacca tattgccgtc ttttggcaat gtgagggccc 120

ggaaacctgg ccctgtcttc ttgacgagca ttcctagggg tctttccccct ctcgccaaag 180

gaatgcaagg tctgttgaat gtcgtgaagg aagcagttcc tctggaagct tcttgaagac 240

aaacaacgtc tgtagcgacc ctttgcaggc agcggaaccc cccacctggc gacaggtgcc 300

tctgcggcca aaagccacgt gtataagata cacctgcaaa ggcggcacaa ccccagtgcc 360

acgttgtgag ttggatagtt gtggaaagag tcaaatggct ctcctcaagc gtattcaaca 420

aggggctgaa ggatgcccag aaggtacccc attgtatggg atctgatctg gggcctcggt 480

gcacatgctt tacatgtgtt tagtcgaggt taaaaaacgt ctaggccccc cgaaccacgg 540

ggacgtggtt ttcctttgaa aaacacgatc 570

<210> 50
<211> 1210
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Epidermal growth factor receptor (EGFR) isoform a
precursor sequence

<400> 50
Met Arg Pro Ser Gly Thr Ala Gly Ala Ala Leu Leu Ala Leu Leu Ala
1 5 10 15

Ala Leu Cys Pro Ala Ser Arg Ala Leu Glu Glu Lys Lys Val Cys Gln
20 25 30

Gly Thr Ser Asn Lys Leu Thr Gln Leu Gly Thr Phe Glu Asp His Phe
35 40 45

Leu Ser Leu Gln Arg Met Phe Asn Asn Cys Glu Val Val Leu Gly Asn

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    50                  55                  60

Leu Glu Ile Thr Tyr Val Gln Arg Asn Tyr Asp Leu Ser Phe Leu Lys
65                  70                  75                  80

Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val
                85                  90                  95

Glu Arg Ile Pro Leu Glu Asn Leu Gln Ile Ile Arg Gly Asn Met Tyr
            100                 105                 110

Tyr Glu Asn Ser Tyr Ala Leu Ala Val Leu Ser Asn Tyr Asp Ala Asn
        115                 120                 125

Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu
    130                 135                 140

His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu
145                 150                 155                 160

Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met
                165                 170                 175

Ser Met Asp Phe Gln Asn His Leu Gly Ser Cys Gln Lys Cys Asp Pro
            180                 185                 190

Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln
        195                 200                 205

Lys Leu Thr Lys Ile Ile Cys Ala Gln Gln Cys Ser Gly Arg Cys Arg
    210                 215                 220

Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys
225                 230                 235                 240

Thr Gly Pro Arg Glu Ser Asp Cys Leu Val Cys Arg Lys Phe Arg Asp
                245                 250                 255
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Glu Ala Thr Cys Lys Asp Thr Cys Pro Pro Leu Met Leu Tyr Asn Pro
            260                 265                 270

Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly
        275                 280                 285

Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His
    290                 295                 300

Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu
305                 310                 315                 320

Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val
                325                 330                 335

Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn
            340                 345                 350

Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp
        355                 360                 365

Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr
    370                 375                 380

Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu
385                 390                 395                 400

Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp
                405                 410                 415

Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln
            420                 425                 430

His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu
        435                 440                 445
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Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser
    450                 455                 460

Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu
465                 470                 475                 480

Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu
                485                 490                 495

Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro
            500                 505                 510

Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn
        515                 520                 525

Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly
    530                 535                 540

Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro
545                 550                 555                 560

Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro
                565                 570                 575

Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val
            580                 585                 590

Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp
        595                 600                 605

Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys
    610                 615                 620

Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly
625                 630                 635                 640
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Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu
                645                 650                 655

Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met Arg Arg Arg His
            660                 665                 670

Ile Val Arg Lys Arg Thr Leu Arg Arg Leu Leu Gln Glu Arg Glu Leu
        675                 680                 685

Val Glu Pro Leu Thr Pro Ser Gly Glu Ala Pro Asn Gln Ala Leu Leu
    690                 695                 700

Arg Ile Leu Lys Glu Thr Glu Phe Lys Lys Ile Lys Val Leu Gly Ser
705                 710                 715                 720

Gly Ala Phe Gly Thr Val Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu
                725                 730                 735

Lys Val Lys Ile Pro Val Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser
            740                 745                 750

Pro Lys Ala Asn Lys Glu Ile Leu Asp Glu Ala Tyr Val Met Ala Ser
        755                 760                 765

Val Asp Asn Pro His Val Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser
    770                 775                 780

Thr Val Gln Leu Ile Thr Gln Leu Met Pro Phe Gly Cys Leu Leu Asp
785                 790                 795                 800

Tyr Val Arg Glu His Lys Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn
                805                 810                 815

Trp Cys Val Gln Ile Ala Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg
            820                 825                 830

Leu Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Lys Thr Pro
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        835                 840                 845

Gln His Val Lys Ile Thr Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala
    850                 855                 860

Glu Glu Lys Glu Tyr His Ala Glu Gly Gly Lys Val Pro Ile Lys Trp
865                 870                 875                 880

Met Ala Leu Glu Ser Ile Leu His Arg Ile Tyr Thr His Gln Ser Asp
                885                 890                 895

Val Trp Ser Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ser
            900                 905                 910

Lys Pro Tyr Asp Gly Ile Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu
        915                 920                 925

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
    930                 935                 940

Met Ile Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
945                 950                 955                 960

Phe Arg Glu Leu Ile Ile Glu Phe Ser Lys Met Ala Arg Asp Pro Gln
                965                 970                 975

Arg Tyr Leu Val Ile Gln Gly Asp Glu Arg Met His Leu Pro Ser Pro
            980                 985                 990

Thr Asp Ser Asn Phe Tyr Arg Ala  Leu Met Asp Glu Glu  Asp Met Asp
        995                 1000                1005

Asp Val  Val Asp Ala Asp Glu  Tyr Leu Ile Pro Gln  Gln Gly Phe
    1010                1015                1020

Phe Ser  Ser Pro Ser Thr Ser  Arg Thr Pro Leu Leu  Ser Ser Leu
    1025                1030                1035
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Ser Ala  Thr Ser Asn Asn Ser  Thr Val Ala Cys Ile  Asp Arg Asn
    1040                1045                1050

Gly Leu  Gln Ser Cys Pro Ile  Lys Glu Asp Ser Phe  Leu Gln Arg
    1055                1060                1065

Tyr Ser  Ser Asp Pro Thr Gly  Ala Leu Thr Glu Asp  Ser Ile Asp
    1070                1075                1080

Asp Thr  Phe Leu Pro Val Pro  Glu Tyr Ile Asn Gln  Ser Val Pro
    1085                1090                1095

Lys Arg  Pro Ala Gly Ser Val  Gln Asn Pro Val Tyr  His Asn Gln
    1100                1105                1110

Pro Leu  Asn Pro Ala Pro Ser  Arg Asp Pro His Tyr  Gln Asp Pro
    1115                1120                1125

His Ser  Thr Ala Val Gly Asn  Pro Glu Tyr Leu Asn  Thr Val Gln
    1130                1135                1140

Pro Thr  Cys Val Asn Ser Thr  Phe Asp Ser Pro Ala  His Trp Ala
    1145                1150                1155

Gln Lys  Gly Ser His Gln Ile  Ser Leu Asp Asn Pro  Asp Tyr Gln
    1160                1165                1170

Gln Asp  Phe Phe Pro Lys Glu  Ala Lys Pro Asn Gly  Ile Phe Lys
    1175                1180                1185

Gly Ser  Thr Ala Glu Asn Ala  Glu Tyr Leu Arg Val  Ala Pro Gln
    1190                1195                1200

Ser Ser  Glu Phe Ile Gly Ala
    1205                1210
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<210> 51
<211> 1255
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Receptor tyrosine-protein kinase ErbB2 (HER2) isoform a
precursor sequence

<400> 51
Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu
1 5 10 15

Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Met Lys
20 25 30

Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His
35 40 45

Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr
50 55 60

Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val
65 70 75 80

Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu
85 90 95

Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr
100 105 110

Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Asn Asn Thr Thr Pro
115 120 125

Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser
130 135 140

Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln

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145                 150                 155                 160

Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn
                165                 170                 175

Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys
            180                 185                 190

His Pro Cys Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser
        195                 200                 205

Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys
    210                 215                 220

Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
225                 230                 235                 240

Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu
                245                 250                 255

His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val
            260                 265                 270

Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg
        275                 280                 285

Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu
    290                 295                 300

Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln
305                 310                 315                 320

Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys
                325                 330                 335

Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu
            340                 345                 350
```

```
Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys
        355                 360                 365

Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp
    370                 375                 380

Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Gln Val Phe
385                 390                 395                 400

Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro
                405                 410                 415

Asp Ser Leu Pro Asp Leu Ser Val Phe Gln Asn Leu Gln Val Ile Arg
            420                 425                 430

Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
        435                 440                 445

Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
    450                 455                 460

Leu Ala Leu Ile His His Asn Thr His Leu Cys Phe Val His Thr Val
465                 470                 475                 480

Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
                485                 490                 495

Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
            500                 505                 510

Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
        515                 520                 525

Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
    530                 535                 540
```

```
Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
545                 550                 555                 560

Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
                565                 570                 575

Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
            580                 585                 590

Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
        595                 600                 605

Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln
    610                 615                 620

Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
625                 630                 635                 640

Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
                645                 650                 655

Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
            660                 665                 670

Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
        675                 680                 685

Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
    690                 695                 700

Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
705                 710                 715                 720

Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
                725                 730                 735
```

```
Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
            740                 745                 750

Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
        755                 760                 765

Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
    770                 775                 780

Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
785                 790                 795                 800

Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg
                805                 810                 815

Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala Lys Gly
            820                 825                 830

Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu Ala Ala
        835                 840                 845

Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe
    850                 855                 860

Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His Ala Asp
865                 870                 875                 880

Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile Leu Arg
                885                 890                 895

Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Val
            900                 905                 910

Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile Pro Ala
        915                 920                 925

Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro
```

```
    930                 935                 940

Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys Trp Met
945                 950                 955                 960

Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser Glu Phe
                965                 970                 975

Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln Asn Glu
            980                 985                 990

Asp Leu Gly Pro Ala Ser Pro Leu  Asp Ser Thr Phe Tyr  Arg Ser Leu
        995                 1000                1005

Leu Glu  Asp Asp Asp Met Gly  Asp Leu Val Asp Ala  Glu Glu Tyr
    1010                1015                1020

Leu Val  Pro Gln Gln Gly Phe  Phe Cys Pro Asp Pro  Ala Pro Gly
    1025                1030                1035

Ala Gly  Gly Met Val His His  Arg His Arg Ser Ser  Ser Thr Arg
    1040                1045                1050

Ser Gly  Gly Gly Asp Leu Thr  Leu Gly Leu Glu Pro  Ser Glu Glu
    1055                1060                1065

Glu Ala  Pro Arg Ser Pro Leu  Ala Pro Ser Glu Gly  Ala Gly Ser
    1070                1075                1080

Asp Val  Phe Asp Gly Asp Leu  Gly Met Gly Ala Ala  Lys Gly Leu
    1085                1090                1095

Gln Ser  Leu Pro Thr His Asp  Pro Ser Pro Leu Gln  Arg Tyr Ser
    1100                1105                1110

Glu Asp  Pro Thr Val Pro Leu  Pro Ser Glu Thr Asp  Gly Tyr Val
    1115                1120                1125
```

```
Ala Pro  Leu Thr Cys Ser Pro  Gln Pro Glu Tyr Val  Asn Gln Pro
    1130                1135                1140


Asp Val  Arg Pro Gln Pro Pro  Ser Pro Arg Glu Gly  Pro Leu Pro
    1145                1150                1155


Ala Ala  Arg Pro Ala Gly Ala  Thr Leu Glu Arg Pro  Lys Thr Leu
    1160                1165                1170


Ser Pro  Gly Lys Asn Gly Val  Val Lys Asp Val Phe  Ala Phe Gly
    1175                1180                1185


Gly Ala  Val Glu Asn Pro Glu  Tyr Leu Thr Pro Gln  Gly Gly Ala
    1190                1195                1200


Ala Pro  Gln Pro His Pro Pro  Pro Ala Phe Ser Pro  Ala Phe Asp
    1205                1210                1215


Asn Leu  Tyr Tyr Trp Asp Gln  Asp Pro Pro Glu Arg  Gly Ala Pro
    1220                1225                1230


Pro Ser  Thr Phe Lys Gly Thr  Pro Thr Ala Glu Asn  Pro Glu Tyr
    1235                1240                1245


Leu Gly  Leu Asp Val Pro Val
    1250                1255
```

<210> 52
<211> 1342
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Receptor tyrosine-protein kinase ErbB3 (HER3) isoform 1 precursor sequence

<400> 52

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Met Arg Ala Asn Asp Ala Leu Gln Val Leu Gly Leu Leu Phe Ser Leu
1               5                  10                  15

Ala Arg Gly Ser Glu Val Gly Asn Ser Gln Ala Val Cys Pro Gly Thr
            20                  25                  30

Leu Asn Gly Leu Ser Val Thr Gly Asp Ala Glu Asn Gln Tyr Gln Thr
        35                  40                  45

Leu Tyr Lys Leu Tyr Glu Arg Cys Glu Val Val Met Gly Asn Leu Glu
    50                  55                  60

Ile Val Leu Thr Gly His Asn Ala Asp Leu Ser Phe Leu Gln Trp Ile
65                  70                  75                  80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Met Asn Glu Phe Ser Thr
                85                  90                  95

Leu Pro Leu Pro Asn Leu Arg Val Val Arg Gly Thr Gln Val Tyr Asp
            100                 105                 110

Gly Lys Phe Ala Ile Phe Val Met Leu Asn Tyr Asn Thr Asn Ser Ser
        115                 120                 125

His Ala Leu Arg Gln Leu Arg Leu Thr Gln Leu Thr Glu Ile Leu Ser
    130                 135                 140

Gly Gly Val Tyr Ile Glu Lys Asn Asp Lys Leu Cys His Met Asp Thr
145                 150                 155                 160

Ile Asp Trp Arg Asp Ile Val Arg Asp Arg Asp Ala Glu Ile Val Val
                165                 170                 175

Lys Asp Asn Gly Arg Ser Cys Pro Pro Cys His Glu Val Cys Lys Gly
            180                 185                 190

Arg Cys Trp Gly Pro Gly Ser Glu Asp Cys Gln Thr Leu Thr Lys Thr
```

```
        195                 200                 205

Ile Cys Ala Pro Gln Cys Asn Gly His Cys Phe Gly Pro Asn Pro Asn
    210                 215                 220

Gln Cys Cys His Asp Glu Cys Ala Gly Gly Cys Ser Gly Pro Gln Asp
225                 230                 235                 240

Thr Asp Cys Phe Ala Cys Arg His Phe Asn Asp Ser Gly Ala Cys Val
                245                 250                 255

Pro Arg Cys Pro Gln Pro Leu Val Tyr Asn Lys Leu Thr Phe Gln Leu
            260                 265                 270

Glu Pro Asn Pro His Thr Lys Tyr Gln Tyr Gly Gly Val Cys Val Ala
        275                 280                 285

Ser Cys Pro His Asn Phe Val Val Asp Gln Thr Ser Cys Val Arg Ala
    290                 295                 300

Cys Pro Pro Asp Lys Met Glu Val Asp Lys Asn Gly Leu Lys Met Cys
305                 310                 315                 320

Glu Pro Cys Gly Gly Leu Cys Pro Lys Ala Cys Glu Gly Thr Gly Ser
                325                 330                 335

Gly Ser Arg Phe Gln Thr Val Asp Ser Ser Asn Ile Asp Gly Phe Val
            340                 345                 350

Asn Cys Thr Lys Ile Leu Gly Asn Leu Asp Phe Leu Ile Thr Gly Leu
        355                 360                 365

Asn Gly Asp Pro Trp His Lys Ile Pro Ala Leu Asp Pro Glu Lys Leu
    370                 375                 380

Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly Tyr Leu Asn Ile Gln
385                 390                 395                 400
```

```
Ser Trp Pro Pro His Met His Asn Phe Ser Val Phe Ser Asn Leu Thr
                405                 410                 415

Thr Ile Gly Gly Arg Ser Leu Tyr Asn Arg Gly Phe Ser Leu Leu Ile
            420                 425                 430

Met Lys Asn Leu Asn Val Thr Ser Leu Gly Phe Arg Ser Leu Lys Glu
        435                 440                 445

Ile Ser Ala Gly Arg Ile Tyr Ile Ser Ala Asn Arg Gln Leu Cys Tyr
    450                 455                 460

His His Ser Leu Asn Trp Thr Lys Val Leu Arg Gly Pro Thr Glu Glu
465                 470                 475                 480

Arg Leu Asp Ile Lys His Asn Arg Pro Arg Arg Asp Cys Val Ala Glu
                485                 490                 495

Gly Lys Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro
            500                 505                 510

Gly Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val
        515                 520                 525

Cys Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala
    530                 535                 540

His Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu
545                 550                 555                 560

Gly Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys
                565                 570                 575

Ala His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly
            580                 585                 590
```

```
Val Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn
        595                 600                 605

Glu Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro
    610                 615                 620

Glu Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr
625                 630                 635                 640

His Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe
                645                 650                 655

Met Met Leu Gly Gly Thr Phe Leu Tyr Trp Arg Gly Arg Arg Ile Gln
            660                 665                 670

Asn Lys Arg Ala Met Arg Arg Tyr Leu Glu Arg Gly Glu Ser Ile Glu
        675                 680                 685

Pro Leu Asp Pro Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe
    690                 695                 700

Lys Glu Thr Glu Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe
705                 710                 715                 720

Gly Thr Val His Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys
                725                 730                 735

Ile Pro Val Cys Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser
            740                 745                 750

Phe Gln Ala Val Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His
        755                 760                 765

Ala His Ile Val Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln
    770                 775                 780
```

```
Leu Val Thr Gln Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg
785                 790                 795                 800

Gln His Arg Gly Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val
                805                 810                 815

Gln Ile Ala Lys Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His
            820                 825                 830

Arg Asn Leu Ala Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val
        835                 840                 845

Gln Val Ala Asp Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys
    850                 855                 860

Gln Leu Leu Tyr Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu
865                 870                 875                 880

Glu Ser Ile His Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser
                885                 890                 895

Tyr Gly Val Thr Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr
            900                 905                 910

Ala Gly Leu Arg Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu
        915                 920                 925

Arg Leu Ala Gln Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met
    930                 935                 940

Val Lys Cys Trp Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu
945                 950                 955                 960

Leu Ala Asn Glu Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu
                965                 970                 975

Val Ile Lys Arg Glu Ser Gly Pro Gly Ile Ala Pro Gly Pro Glu Pro
```

```
           980                 985                 990

His Gly Leu Thr Asn Lys Lys Leu  Glu Glu Val Glu Leu  Glu Pro Glu
        995                1000                1005

Leu Asp  Leu Asp Leu Asp Leu  Glu Ala Glu Glu Asp  Asn Leu Ala
    1010                1015                1020

Thr Thr  Thr Leu Gly Ser Ala  Leu Ser Leu Pro Val  Gly Thr Leu
    1025                1030                1035

Asn Arg  Pro Arg Gly Ser Gln  Ser Leu Leu Ser Pro  Ser Ser Gly
    1040                1045                1050

Tyr Met  Pro Met Asn Gln Gly  Asn Leu Gly Glu Ser  Cys Gln Glu
    1055                1060                1065

Ser Ala  Val Ser Gly Ser Ser  Glu Arg Cys Pro Arg  Pro Val Ser
    1070                1075                1080

Leu His  Pro Met Pro Arg Gly  Cys Leu Ala Ser Glu  Ser Ser Glu
    1085                1090                1095

Gly His  Val Thr Gly Ser Glu  Ala Glu Leu Gln Glu  Lys Val Ser
    1100                1105                1110

Met Cys  Arg Ser Arg Ser Arg  Ser Arg Ser Pro Arg  Pro Arg Gly
    1115                1120                1125

Asp Ser  Ala Tyr His Ser Gln  Arg His Ser Leu Leu  Thr Pro Val
    1130                1135                1140

Thr Pro  Leu Ser Pro Pro Gly  Leu Glu Glu Glu Asp  Val Asn Gly
    1145                1150                1155

Tyr Val  Met Pro Asp Thr His  Leu Lys Gly Thr Pro  Ser Ser Arg
    1160                1165                1170
```

```
Glu Gly  Thr Leu Ser Ser Val  Gly Leu Ser Ser Val  Leu Gly Thr
    1175                1180                1185

Glu Glu  Glu Asp Glu Asp Glu  Glu Tyr Glu Tyr Met  Asn Arg Arg
    1190                1195                1200

Arg Arg  His Ser Pro Pro His  Pro Pro Arg Pro Ser  Ser Leu Glu
    1205                1210                1215

Glu Leu  Gly Tyr Glu Tyr Met  Asp Val Gly Ser Asp  Leu Ser Ala
    1220                1225                1230

Ser Leu  Gly Ser Thr Gln Ser  Cys Pro Leu His Pro  Val Pro Ile
    1235                1240                1245

Met Pro  Thr Ala Gly Thr Thr  Pro Asp Glu Asp Tyr  Glu Tyr Met
    1250                1255                1260

Asn Arg  Gln Arg Asp Gly Gly  Gly Pro Gly Gly Asp  Tyr Ala Ala
    1265                1270                1275

Met Gly  Ala Cys Pro Ala Ser  Glu Gln Gly Tyr Glu  Glu Met Arg
    1280                1285                1290

Ala Phe  Gln Gly Pro Gly His  Gln Ala Pro His Val  His Tyr Ala
    1295                1300                1305

Arg Leu  Lys Thr Leu Arg Ser  Leu Glu Ala Thr Asp  Ser Ala Phe
    1310                1315                1320

Asp Asn  Pro Asp Tyr Trp His  Ser Arg Leu Phe Pro  Lys Ala Asn
    1325                1330                1335

Ala Gln  Arg Thr
    1340
```

<210> 53
<211> 1308
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Receptor tyrosine-protein kinase ErbB4 (HER4) isoform
JM-a/CVT-1 precursor sequence

<400> 53
Met Lys Pro Ala Thr Gly Leu Trp Val Trp Val Ser Leu Leu Val Ala
1 5 10 15

Ala Gly Thr Val Gln Pro Ser Asp Ser Gln Ser Val Cys Ala Gly Thr
20 25 30

Glu Asn Lys Leu Ser Ser Leu Ser Asp Leu Glu Gln Gln Tyr Arg Ala
35 40 45

Leu Arg Lys Tyr Tyr Glu Asn Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Thr Ser Ile Glu His Asn Arg Asp Leu Ser Phe Leu Arg Ser Val
65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Leu Asn Gln Phe Arg Tyr
85 90 95

Leu Pro Leu Glu Asn Leu Arg Ile Ile Arg Gly Thr Lys Leu Tyr Glu
100 105 110

Asp Arg Tyr Ala Leu Ala Ile Phe Leu Asn Tyr Arg Lys Asp Gly Asn
115 120 125

Phe Gly Leu Gln Glu Leu Gly Leu Lys Asn Leu Thr Glu Ile Leu Asn
130 135 140

Gly Gly Val Tyr Val Asp Gln Asn Lys Phe Leu Cys Tyr Ala Asp Thr

```
145                 150                 155                 160

Ile His Trp Gln Asp Ile Val Arg Asn Pro Trp Pro Ser Asn Leu Thr
                165                 170                 175

Leu Val Ser Thr Asn Gly Ser Ser Gly Cys Gly Arg Cys His Lys Ser
            180                 185                 190

Cys Thr Gly Arg Cys Trp Gly Pro Thr Glu Asn His Cys Gln Thr Leu
        195                 200                 205

Thr Arg Thr Val Cys Ala Glu Gln Cys Asp Gly Arg Cys Tyr Gly Pro
    210                 215                 220

Tyr Val Ser Asp Cys Cys His Arg Glu Cys Ala Gly Gly Cys Ser Gly
225                 230                 235                 240

Pro Lys Asp Thr Asp Cys Phe Ala Cys Met Asn Phe Asn Asp Ser Gly
                245                 250                 255

Ala Cys Val Thr Gln Cys Pro Gln Thr Phe Val Tyr Asn Pro Thr Thr
            260                 265                 270

Phe Gln Leu Glu His Asn Phe Asn Ala Lys Tyr Thr Tyr Gly Ala Phe
        275                 280                 285

Cys Val Lys Lys Cys Pro His Asn Phe Val Val Asp Ser Ser Ser Cys
    290                 295                 300

Val Arg Ala Cys Pro Ser Ser Lys Met Glu Val Glu Glu Asn Gly Ile
305                 310                 315                 320

Lys Met Cys Lys Pro Cys Thr Asp Ile Cys Pro Lys Ala Cys Asp Gly
                325                 330                 335

Ile Gly Thr Gly Ser Leu Met Ser Ala Gln Thr Val Asp Ser Ser Asn
            340                 345                 350
```

```
Ile Asp Lys Phe Ile Asn Cys Thr Lys Ile Asn Gly Asn Leu Ile Phe
        355                 360                 365

Leu Val Thr Gly Ile His Gly Asp Pro Tyr Asn Ala Ile Glu Ala Ile
    370                 375                 380

Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
385                 390                 395                 400

Phe Leu Asn Ile Gln Ser Trp Pro Pro Asn Met Thr Asp Phe Ser Val
                405                 410                 415

Phe Ser Asn Leu Val Thr Ile Gly Gly Arg Val Leu Tyr Ser Gly Leu
            420                 425                 430

Ser Leu Leu Ile Leu Lys Gln Gln Gly Ile Thr Ser Leu Gln Phe Gln
        435                 440                 445

Ser Leu Lys Glu Ile Ser Ala Gly Asn Ile Tyr Ile Thr Asp Asn Ser
    450                 455                 460

Asn Leu Cys Tyr Tyr His Thr Ile Asn Trp Thr Thr Leu Phe Ser Thr
465                 470                 475                 480

Ile Asn Gln Arg Ile Val Ile Arg Asp Asn Arg Lys Ala Glu Asn Cys
                485                 490                 495

Thr Ala Glu Gly Met Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys
            500                 505                 510

Trp Gly Pro Gly Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg
        515                 520                 525

Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu Tyr Asp Gly Glu Phe Arg
    530                 535                 540
```

```
Glu Phe Glu Asn Gly Ser Ile Cys Val Glu Cys Asp Pro Gln Cys Glu
545                 550                 555                 560

Lys Met Glu Asp Gly Leu Leu Thr Cys His Gly Pro Gly Pro Asp Asn
                565                 570                 575

Cys Thr Lys Cys Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu Lys
            580                 585                 590

Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr Ala
        595                 600                 605

Asp Pro Asp Arg Glu Cys His Pro Cys His Pro Asn Cys Thr Gln Gly
    610                 615                 620

Cys Asn Gly Pro Thr Ser His Asp Cys Ile Tyr Tyr Pro Trp Thr Gly
625                 630                 635                 640

His Ser Thr Leu Pro Gln His Ala Arg Thr Pro Leu Ile Ala Ala Gly
                645                 650                 655

Val Ile Gly Gly Leu Phe Ile Leu Val Ile Val Gly Leu Thr Phe Ala
            660                 665                 670

Val Tyr Val Arg Arg Lys Ser Ile Lys Lys Lys Arg Ala Leu Arg Arg
        675                 680                 685

Phe Leu Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly Thr Ala
    690                 695                 700

Pro Asn Gln Ala Gln Leu Arg Ile Leu Lys Glu Thr Glu Leu Lys Arg
705                 710                 715                 720

Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys Gly Ile
                725                 730                 735
```

```
Trp Val Pro Glu Gly Glu Thr Val Lys Ile Pro Val Ala Ile Lys Ile
            740                 745                 750

Leu Asn Glu Thr Thr Gly Pro Lys Ala Asn Val Glu Phe Met Asp Glu
        755                 760                 765

Ala Leu Ile Met Ala Ser Met Asp His Pro His Leu Val Arg Leu Leu
    770                 775                 780

Gly Val Cys Leu Ser Pro Thr Ile Gln Leu Val Thr Gln Leu Met Pro
785                 790                 795                 800

His Gly Cys Leu Leu Glu Tyr Val His Glu His Lys Asp Asn Ile Gly
                805                 810                 815

Ser Gln Leu Leu Leu Asn Trp Cys Val Gln Ile Ala Lys Gly Met Met
            820                 825                 830

Tyr Leu Glu Glu Arg Arg Leu Val His Arg Asp Leu Ala Ala Arg Asn
        835                 840                 845

Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr Asp Phe Gly Leu
    850                 855                 860

Ala Arg Leu Leu Glu Gly Asp Glu Lys Glu Tyr Asn Ala Asp Gly Gly
865                 870                 875                 880

Lys Met Pro Ile Lys Trp Met Ala Leu Glu Cys Ile His Tyr Arg Lys
                885                 890                 895

Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr Ile Trp Glu
            900                 905                 910

Leu Met Thr Phe Gly Gly Lys Pro Tyr Asp Gly Ile Pro Thr Arg Glu
        915                 920                 925

Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile
```

```
    930                 935                 940

Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp Met Ile Asp
945                 950                 955                 960

Ala Asp Ser Arg Pro Lys Phe Lys Glu Leu Ala Ala Glu Phe Ser Arg
                965                 970                 975

Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln Gly Asp Asp Arg
            980                 985                 990

Met Lys Leu Pro Ser Pro Asn Asp  Ser Lys Phe Phe Gln  Asn Leu Leu
        995                 1000                1005

Asp Glu  Glu Asp Leu Glu Asp  Met Met Asp Ala Glu  Glu Tyr Leu
    1010                1015                1020

Val Pro  Gln Ala Phe Asn Ile  Pro Pro Pro Ile Tyr  Thr Ser Arg
    1025                1030                1035

Ala Arg  Ile Asp Ser Asn Arg  Ser Glu Ile Gly His  Ser Pro Pro
    1040                1045                1050

Pro Ala  Tyr Thr Pro Met Ser  Gly Asn Gln Phe Val  Tyr Arg Asp
    1055                1060                1065

Gly Gly  Phe Ala Ala Glu Gln  Gly Val Ser Val Pro  Tyr Arg Ala
    1070                1075                1080

Pro Thr  Ser Thr Ile Pro Glu  Ala Pro Val Ala Gln  Gly Ala Thr
    1085                1090                1095

Ala Glu  Ile Phe Asp Asp Ser  Cys Cys Asn Gly Thr  Leu Arg Lys
    1100                1105                1110

Pro Val  Ala Pro His Val Gln  Glu Asp Ser Ser Thr  Gln Arg Tyr
    1115                1120                1125
```

```
Ser Ala  Asp Pro Thr Val Phe  Ala Pro Glu Arg Ser  Pro Arg Gly
    1130                1135                1140

Glu Leu  Asp Glu Glu Gly Tyr  Met Thr Pro Met Arg  Asp Lys Pro
    1145                1150                1155

Lys Gln  Glu Tyr Leu Asn Pro  Val Glu Glu Asn Pro  Phe Val Ser
    1160                1165                1170

Arg Arg  Lys Asn Gly Asp Leu  Gln Ala Leu Asp Asn  Pro Glu Tyr
    1175                1180                1185

His Asn  Ala Ser Asn Gly Pro  Pro Lys Ala Glu Asp  Glu Tyr Val
    1190                1195                1200

Asn Glu  Pro Leu Tyr Leu Asn  Thr Phe Ala Asn Thr  Leu Gly Lys
    1205                1210                1215

Ala Glu  Tyr Leu Lys Asn Asn  Ile Leu Ser Met Pro  Glu Lys Ala
    1220                1225                1230

Lys Lys  Ala Phe Asp Asn Pro  Asp Tyr Trp Asn His  Ser Leu Pro
    1235                1240                1245

Pro Arg  Ser Thr Leu Gln His  Pro Asp Tyr Leu Gln  Glu Tyr Ser
    1250                1255                1260

Thr Lys  Tyr Phe Tyr Lys Gln  Asn Gly Arg Ile Arg  Pro Ile Val
    1265                1270                1275

Ala Glu  Asn Pro Glu Tyr Leu  Ser Glu Phe Ser Leu  Lys Pro Gly
    1280                1285                1290

Thr Val  Leu Pro Pro Pro Pro  Tyr Arg His Arg Asn  Thr Val Val
    1295                1300                1305
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<210> 54
<211> 1298
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Receptor tyrosine-protein kinase ErbB4 (HER4) isoform JM-b
(isoform X7) precursor sequence

<400> 54
Met Lys Pro Ala Thr Gly Leu Trp Val Trp Val Ser Leu Leu Val Ala
1 5 10 15

Ala Gly Thr Val Gln Pro Ser Asp Ser Gln Ser Val Cys Ala Gly Thr
20 25 30

Glu Asn Lys Leu Ser Ser Leu Ser Asp Leu Glu Gln Gln Tyr Arg Ala
35 40 45

Leu Arg Lys Tyr Tyr Glu Asn Cys Glu Val Val Met Gly Asn Leu Glu
50 55 60

Ile Thr Ser Ile Glu His Asn Arg Asp Leu Ser Phe Leu Arg Ser Val
65 70 75 80

Arg Glu Val Thr Gly Tyr Val Leu Val Ala Leu Asn Gln Phe Arg Tyr
85 90 95

Leu Pro Leu Glu Asn Leu Arg Ile Ile Arg Gly Thr Lys Leu Tyr Glu
100 105 110

Asp Arg Tyr Ala Leu Ala Ile Phe Leu Asn Tyr Arg Lys Asp Gly Asn
115 120 125

Phe Gly Leu Gln Glu Leu Gly Leu Lys Asn Leu Thr Glu Ile Leu Asn
130 135 140

Gly Gly Val Tyr Val Asp Gln Asn Lys Phe Leu Cys Tyr Ala Asp Thr

```
145                 150                 155                 160

Ile His Trp Gln Asp Ile Val Arg Asn Pro Trp Pro Ser Asn Leu Thr
                165                 170                 175

Leu Val Ser Thr Asn Gly Ser Ser Gly Cys Gly Arg Cys His Lys Ser
            180                 185                 190

Cys Thr Gly Arg Cys Trp Gly Pro Thr Glu Asn His Cys Gln Thr Leu
        195                 200                 205

Thr Arg Thr Val Cys Ala Glu Gln Cys Asp Gly Arg Cys Tyr Gly Pro
    210                 215                 220

Tyr Val Ser Asp Cys Cys His Arg Glu Cys Ala Gly Gly Cys Ser Gly
225                 230                 235                 240

Pro Lys Asp Thr Asp Cys Phe Ala Cys Met Asn Phe Asn Asp Ser Gly
                245                 250                 255

Ala Cys Val Thr Gln Cys Pro Gln Thr Phe Val Tyr Asn Pro Thr Thr
            260                 265                 270

Phe Gln Leu Glu His Asn Phe Asn Ala Lys Tyr Thr Tyr Gly Ala Phe
        275                 280                 285

Cys Val Lys Lys Cys Pro His Asn Phe Val Val Asp Ser Ser Ser Cys
    290                 295                 300

Val Arg Ala Cys Pro Ser Ser Lys Met Glu Val Glu Glu Asn Gly Ile
305                 310                 315                 320

Lys Met Cys Lys Pro Cys Thr Asp Ile Cys Pro Lys Ala Cys Asp Gly
                325                 330                 335

Ile Gly Thr Gly Ser Leu Met Ser Ala Gln Thr Val Asp Ser Ser Asn
            340                 345                 350
```

```
Ile Asp Lys Phe Ile Asn Cys Thr Lys Ile Asn Gly Asn Leu Ile Phe
        355                 360                 365

Leu Val Thr Gly Ile His Gly Asp Pro Tyr Asn Ala Ile Glu Ala Ile
    370                 375                 380

Asp Pro Glu Lys Leu Asn Val Phe Arg Thr Val Arg Glu Ile Thr Gly
385                 390                 395                 400

Phe Leu Asn Ile Gln Ser Trp Pro Pro Asn Met Thr Asp Phe Ser Val
                405                 410                 415

Phe Ser Asn Leu Val Thr Ile Gly Gly Arg Val Leu Tyr Ser Gly Leu
            420                 425                 430

Ser Leu Leu Ile Leu Lys Gln Gln Gly Ile Thr Ser Leu Gln Phe Gln
        435                 440                 445

Ser Leu Lys Glu Ile Ser Ala Gly Asn Ile Tyr Ile Thr Asp Asn Ser
    450                 455                 460

Asn Leu Cys Tyr Tyr His Thr Ile Asn Trp Thr Thr Leu Phe Ser Thr
465                 470                 475                 480

Ile Asn Gln Arg Ile Val Ile Arg Asp Asn Arg Lys Ala Glu Asn Cys
                485                 490                 495

Thr Ala Glu Gly Met Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys
            500                 505                 510

Trp Gly Pro Gly Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg
        515                 520                 525

Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu Tyr Asp Gly Glu Phe Arg
    530                 535                 540
```

```
Glu Phe Glu Asn Gly Ser Ile Cys Val Glu Cys Asp Pro Gln Cys Glu
545                 550                 555                 560

Lys Met Glu Asp Gly Leu Leu Thr Cys His Gly Pro Gly Pro Asp Asn
                565                 570                 575

Cys Thr Lys Cys Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu Lys
            580                 585                 590

Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr Ala
        595                 600                 605

Asp Pro Asp Arg Glu Cys His Pro Cys His Pro Asn Cys Thr Gln Gly
    610                 615                 620

Cys Ile Gly Ser Ser Ile Glu Asp Cys Ile Gly Leu Met Asp Arg Thr
625                 630                 635                 640

Pro Leu Ile Ala Ala Gly Val Ile Gly Gly Leu Phe Ile Leu Val Ile
                645                 650                 655

Val Gly Leu Thr Phe Ala Val Tyr Val Arg Arg Lys Ser Ile Lys Lys
            660                 665                 670

Lys Arg Ala Leu Arg Arg Phe Leu Glu Thr Glu Leu Val Glu Pro Leu
        675                 680                 685

Thr Pro Ser Gly Thr Ala Pro Asn Gln Ala Gln Leu Arg Ile Leu Lys
    690                 695                 700

Glu Thr Glu Leu Lys Arg Val Lys Val Leu Gly Ser Gly Ala Phe Gly
705                 710                 715                 720

Thr Val Tyr Lys Gly Ile Trp Val Pro Glu Gly Glu Thr Val Lys Ile
                725                 730                 735
```

```
Pro Val Ala Ile Lys Ile Leu Asn Glu Thr Thr Gly Pro Lys Ala Asn
            740                 745                 750

Val Glu Phe Met Asp Glu Ala Leu Ile Met Ala Ser Met Asp His Pro
        755                 760                 765

His Leu Val Arg Leu Leu Gly Val Cys Leu Ser Pro Thr Ile Gln Leu
    770                 775                 780

Val Thr Gln Leu Met Pro His Gly Cys Leu Leu Glu Tyr Val His Glu
785                 790                 795                 800

His Lys Asp Asn Ile Gly Ser Gln Leu Leu Leu Asn Trp Cys Val Gln
                805                 810                 815

Ile Ala Lys Gly Met Met Tyr Leu Glu Glu Arg Arg Leu Val His Arg
            820                 825                 830

Asp Leu Ala Ala Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys
        835                 840                 845

Ile Thr Asp Phe Gly Leu Ala Arg Leu Leu Glu Gly Asp Glu Lys Glu
    850                 855                 860

Tyr Asn Ala Asp Gly Gly Lys Met Pro Ile Lys Trp Met Ala Leu Glu
865                 870                 875                 880

Cys Ile His Tyr Arg Lys Phe Thr His Gln Ser Asp Val Trp Ser Tyr
                885                 890                 895

Gly Val Thr Ile Trp Glu Leu Met Thr Phe Gly Gly Lys Pro Tyr Asp
            900                 905                 910

Gly Ile Pro Thr Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg
        915                 920                 925

Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Val Met Val
```

```
    930                 935                 940

Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe Lys Glu Leu
945                 950                 955                 960

Ala Ala Glu Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Tyr Leu Val
                965                 970                 975

Ile Gln Gly Asp Asp Arg Met Lys Leu Pro Ser Pro Asn Asp Ser Lys
            980                 985                 990

Phe Phe Gln Asn Leu Leu Asp Glu  Glu Asp Leu Glu Asp  Met Met Asp
        995                 1000                1005

Ala Glu  Glu Tyr Leu Val Pro  Gln Ala Phe Asn Ile  Pro Pro Pro
    1010                1015                1020

Ile Tyr  Thr Ser Arg Ala Arg  Ile Asp Ser Asn Arg  Ser Glu Ile
    1025                1030                1035

Gly His  Ser Pro Pro Pro Ala  Tyr Thr Pro Met Ser  Gly Asn Gln
    1040                1045                1050

Phe Val  Tyr Arg Asp Gly Gly  Phe Ala Ala Glu Gln  Gly Val Ser
    1055                1060                1065

Val Pro  Tyr Arg Ala Pro Thr  Ser Thr Ile Pro Glu  Ala Pro Val
    1070                1075                1080

Ala Gln  Gly Ala Thr Ala Glu  Ile Phe Asp Asp Ser  Cys Cys Asn
    1085                1090                1095

Gly Thr  Leu Arg Lys Pro Val  Ala Pro His Val Gln  Glu Asp Ser
    1100                1105                1110

Ser Thr  Gln Arg Tyr Ser Ala  Asp Pro Thr Val Phe  Ala Pro Glu
    1115                1120                1125
```

```
Arg Ser  Pro Arg Gly Glu Leu  Asp Glu Glu Gly Tyr  Met Thr Pro
    1130                1135                1140

Met Arg  Asp Lys Pro Lys Gln  Glu Tyr Leu Asn Pro  Val Glu Glu
    1145                1150                1155

Asn Pro  Phe Val Ser Arg Arg  Lys Asn Gly Asp Leu  Gln Ala Leu
    1160                1165                1170

Asp Asn  Pro Glu Tyr His Asn  Ala Ser Asn Gly Pro  Pro Lys Ala
    1175                1180                1185

Glu Asp  Glu Tyr Val Asn Glu  Pro Leu Tyr Leu Asn  Thr Phe Ala
    1190                1195                1200

Asn Thr  Leu Gly Lys Ala Glu  Tyr Leu Lys Asn Asn  Ile Leu Ser
    1205                1210                1215

Met Pro  Glu Lys Ala Lys Lys  Ala Phe Asp Asn Pro  Asp Tyr Trp
    1220                1225                1230

Asn His  Ser Leu Pro Pro Arg  Ser Thr Leu Gln His  Pro Asp Tyr
    1235                1240                1245

Leu Gln  Glu Tyr Ser Thr Lys  Tyr Phe Tyr Lys Gln  Asn Gly Arg
    1250                1255                1260

Ile Arg  Pro Ile Val Ala Glu  Asn Pro Glu Tyr Leu  Ser Glu Phe
    1265                1270                1275

Ser Leu  Lys Pro Gly Thr Val  Leu Pro Pro Pro Pro  Tyr Arg His
    1280                1285                1290

Arg Asn  Thr Val Val
    1295
```

<210> 55
<211> 335
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 55
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

```
Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
    210                 215                 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225                 230                 235                 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
                245                 250                 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
            260                 265                 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
        275                 280                 285

Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
    290                 295                 300

Thr Asn Gly Pro Lys Ile Pro Ser Ile Ala Thr Gly Met Val Gly Ala
305                 310                 315                 320

Leu Leu Leu Leu Leu Val Val Ala Leu Gly Ile Gly Leu Phe Met
                325                 330                 335
```

<210> 56
<211> 732
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 56
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt 600

gggtcgggtg gcggcggatc tggtggcggt ggctcgtttt gggtgctggt ggtggttggt 660

ggagtcctgg cttgctatag cttgctagta acagtggcct ttattatttt ctgggtgagg 720

agtaagagga gc 732

<210> 57
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 57
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile

```
            20                  25                  30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
        35                  40                  45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
    50                  55                  60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65                  70                  75                  80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
                85                  90                  95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100                 105                 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
    210                 215                 220
```

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
225 230 235 240

Ser Lys Arg Ser

<210> 58
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 58
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg 600

gaatgcgtgg acaagggtgg cggtggctcg ggcggtggtg ggtcgggtgg cggcggatct 660

ggtggcggtg gctcgttttg ggtgctggtg gtggttggtg gagtcctggc ttgctatagc 720

ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag c 771

<210> 59
<211> 257

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 59
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu

```
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Gly Gly Gly
        195                 200                 205

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
    210                 215                 220

Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
225                 230                 235                 240

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
                245                 250                 255

Ser
```

<210> 60
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 60
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg 600

gaatgcgtgg acaagtgcaa ccttctggag ggtgagccaa gggagtttgt ggagaactct 660

gagtgcatac agggtggcgg tggctcgggc ggtggtgggt cgggtggcgg cggatctggt 720

ggcggtggct cgttttgggt gctggtggtg gttggtggag tcctggcttg ctatagcttg 780

ctagtaacag tggcctttat tattttctgg gtgaggagta agaggagc 828

<210> 61
<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 61
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

```
Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100                 105                 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
    210                 215                 220

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
225                 230                 235                 240

Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
                245                 250                 255

Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
            260                 265                 270

Ser Lys Arg Ser
        275
```

<210> 62
<211> 885
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 62
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg 600

gaatgcgtgg acaagtgcaa ccttctggag ggtgagccaa gggagtttgt ggagaactct 660

gagtgcatac agtgccaccc agagtgcctg cctcaggcca tgaacatcac ctgcacagga 720

cggggaccag acaactgtat ccagggcgga ggcggaagcg gaggcggagg ctccggcgga 780

ggcggaagct tttgggtgct ggtggtggtt ggtggagtcc tggcttgcta tagcttgcta 840

gtaacagtgg cctttattat tttctgggtg aggagtaaga ggagc 885

<210> 63
<211> 295
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 63

```
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1               5                  10                  15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
            20                  25                  30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
        35                  40                  45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
    50                  55                  60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65                  70                  75                  80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
                85                  90                  95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100                 105                 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190
```

```
Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
    210                 215                 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225                 230                 235                 240

Arg Gly Pro Asp Asn Cys Ile Gln Gly Gly Gly Gly Ser Gly Gly Gly
                245                 250                 255

Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly
            260                 265                 270

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
        275                 280                 285

Trp Val Arg Ser Lys Arg Ser
    290                 295
```

<210> 64
<211> 924
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 64
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg 600

gaatgcgtgg acaagtgcaa ccttctggag ggtgagccaa gggagtttgt ggagaactct 660

gagtgcatac agtgccaccc agagtgcctg cctcaggcca tgaacatcac ctgcacagga 720

cggggaccag acaactgtat ccagtgtgcc cactacattg acggccccca ctgcgtcaag 780

accggcggag gcggaagcgg aggcggaggc tccggcggag gcggaagctt ttgggtgctg 840

gtggtggttg gtggagtcct ggcttgctat agcttgctag taacagtggc ctttattatt 900

ttctgggtga ggagtaagag gagc 924

<210> 65
<211> 308
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 65
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

```
Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65                  70                  75                  80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
                85                  90                  95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100                 105                 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
    210                 215                 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225                 230                 235                 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
                245                 250                 255
```

```
His Cys Val Lys Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            260                 265                 270


Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala
        275                 280                 285


Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg
    290                 295                 300


Ser Lys Arg Ser
305
```

<210> 66
<211> 984
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 66

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cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct       60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg      120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat      180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac      240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat      300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc      360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat      420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac      480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag      540

ggctgctggg gcccggagcc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg      600

gaatgcgtgg acaagtgcaa ccttctggag ggtgagccaa gggagtttgt ggagaactct      660

gagtgcatac agtgccaccc agagtgcctg cctcaggcca tgaacatcac ctgcacagga      720
```

cggggaccag acaactgtat ccagtgtgcc cactacattg acggccccca ctgcgtcaag 780

acctgcccgg caggagtcat gggagaaaac aacaccctgg tctggaagta cgcagacgcc 840

ggccatgtgt gccacctggg cggaggcgga agcggaggcg gaggctcctt ttgggtgctg 900

gtggtggttg gtggagtcct ggcttgctat agcttgctag taacagtggc ctttattatt 960

ttctgggtga ggagtaagag gagc 984

<210> 67
<211> 328
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 67
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

```
Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
    210                 215                 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225                 230                 235                 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
                245                 250                 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
            260                 265                 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Gly Gly
        275                 280                 285

Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly
    290                 295                 300
```

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
305 310 315 320

Phe Trp Val Arg Ser Lys Arg Ser
325

<210> 68
<211> 1032
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 68
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctcttgcc ggaatgtcag ccgaggcagg 600

gaatgcgtgg acaagtgcaa ccttctggag ggtgagccaa gggagtttgt ggagaactct 660

gagtgcatac agtgccaccc agagtgcctg cctcaggcca tgaacatcac ctgcacagga 720

cggggaccag acaactgtat ccagtgtgcc cactacattg acggccccca ctgcgtcaag 780

acctgcccgg caggagtcat gggagaaaac aacaccctgg tctggaagta cgcagacgcc 840

ggccatgtgt gccacctgtg ccatccaaac tgcacctacg gatgcactgg gccaggtctt 900

gaaggctgtc caggtggcgg tggcggcgga tctttttggg tgctggtggt ggttggtgga 960

gtcctggctt gctatagctt gctagtaaca gtggccttta ttattttctg ggtgaggagt 1020

aagaggagct aa 1032

<210> 69
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 69
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp

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    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
    210                 215                 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225                 230                 235                 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
                245                 250                 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
            260                 265                 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
        275                 280                 285

Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
    290                 295                 300

Gly Gly Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly
305                 310                 315                 320

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
                325                 330                 335
```

Trp Val Arg Ser Lys Arg Ser
340

<210> 70
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 70
atgaggctcc ctgctcagct cctggggctg ctaatgctct gggtcccagg atccagtggg 60

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 120

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 180

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 240

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 300

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 360

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 420

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 480

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 540

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 600

ggctgctggg gcccggagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt 660

gggtcgggtg gcggcggatc tggtggcggt ggctcggaga taacactcat tatttttggg 720

gtgatggctg gtgttattgg aacgatcctc ttaatttctt acggtattcg ccgaggaggt 780

ggaagc 786

<210> 71
<211> 262
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 71
Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1 5 10 15

Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
20 25 30

Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn
35 40 45

Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg
50 55 60

Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp
65 70 75 80

Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala
85 90 95

Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile
100 105 110

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val
115 120 125

Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
130 135 140

Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn
145 150 155 160

Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys
165 170 175

Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val
180 185 190

Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg
195 200 205

Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Thr Leu Ile Ile Phe Gly
225 230 235 240

Val Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile
245 250 255

Arg Arg Gly Gly Gly Ser
260

<210> 72
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 72
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt 600

gggtcgggtg gcggcggatc tggtggcggt ggctcggaga taacactcat tatttttggg 660

gtgatggctg gtgttattgg aacgatcctc ttaatttctt acggtattcg ccgaggaggt 720

ggaagc 726

<210> 73
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 73
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

```
Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Gly Ser Glu Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly
    210                 215                 220

Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg Gly Gly
225                 230                 235                 240

Gly Ser
```

<210> 74
<211> 777
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 74
atgaggctcc ctgctcagct cctggggctg ctaatgctct gggtcccagg atccagtggg 60

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 120

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 180

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 240

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 300

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 360

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 420

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 480

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 540

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 600

ggctgctggg gcccggagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt 660

gggtcgggtg gcggcggatc tggtggcggt ggctcgataa cactcattat ttttggggtg 720

atggctggtg ttattggaac gatcctctta atttcttacg gtattggagg tggaagc 777

<210> 75
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 75
Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1 5 10 15

Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
20 25 30

Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn
35 40 45

Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg

```
    50                  55                  60

Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp
65                  70                  75                  80

Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala
                85                  90                  95

Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile
            100                 105                 110

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val
        115                 120                 125

Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
    130                 135                 140

Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn
145                 150                 155                 160

Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys
                165                 170                 175

Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val
            180                 185                 190

Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg
        195                 200                 205

Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    210                 215                 220

Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val
225                 230                 235                 240

Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Gly
                245                 250                 255
```

Gly Gly Ser

<210> 76
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 76
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt 600

gggtcgggtg gcggcggatc tggtggcggt ggctcgataa cactcattat ttttggggtg 660

atggctggtg ttattggaac gatcctctta atttcttacg gtattggagg tggaagc 717

<210> 77
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 77
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1   5   10   15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
            20   25   30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
        35   40   45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
    50   55   60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65   70   75   80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
                85   90   95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100   105   110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115   120   125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130   135   140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145   150   155   160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165   170   175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180   185   190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
195 200 205

Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val
210 215 220

Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Gly Gly Gly Ser
225 230 235

<210> 78
<211> 777
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 78
atgaggctcc ctgctcagct cctggggctg ctaatgctct gggtcccagg atccagtggg 60

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 120

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 180

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 240

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 300

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 360

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 420

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 480

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 540

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 600

ggctgctggg gcccggagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt 660

gggtcgggtg gcggcggatc tggtggcggt ggctcgataa cactcattat ttttggggtg 720

atggctggtg ttattggaac gatcctctta gccctgctca tctggggagg tggaagc 777

<210> 79
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 79
Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1 5 10 15

Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
20 25 30

Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn
35 40 45

Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg
50 55 60

Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp
65 70 75 80

Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala
85 90 95

Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile
100 105 110

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val
115 120 125

Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
130 135 140

Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn
145 150 155 160

Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys
165 170 175

Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val
180 185 190

Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg
195 200 205

Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
210 215 220

Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val
225 230 235 240

Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly
245 250 255

Gly Gly Ser

<210> 80
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 80
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt 600

gggtcgggtg gcggcggatc tggtggcggt ggctcgataa cactcattat ttttggggtg 660

atggctggtg ttattggaac gatcctctta gccctgctca tctggggagg tggaagc 717

<210> 81
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 81
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

```
Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100                 105                 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        195                 200                 205

Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val
    210                 215                 220

Ile Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
225                 230                 235
```

<210> 82
<211> 771
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 82
atgaggctcc ctgctcagct cctggggctg ctaatgctct gggtcccagg atccagtggg 60

cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 120

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 180

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 240

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 300

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 360

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 420

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 480

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 540

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 600

ggctgctggg gcccggagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt 660

gggtcgggtg gcggcggatc tggtggcggt ggctcgctct gctacctgct ggatggaatc 720

ctcttcatct atggtgtcat tctcactgcc ttgttcctgg gaggtggaag c 771

<210> 83
<211> 257
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 83
Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1 5 10 15

Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
20 25 30

Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn
35 40 45

Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg
50 55 60

```
Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp
65                  70                  75                  80

Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala
                85                  90                  95

Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile
            100                 105                 110

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val
        115                 120                 125

Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
    130                 135                 140

Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn
145                 150                 155                 160

Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys
                165                 170                 175

Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val
            180                 185                 190

Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg
        195                 200                 205

Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    210                 215                 220

Gly Gly Ser Gly Gly Gly Gly Ser Leu Cys Tyr Leu Leu Asp Gly Ile
225                 230                 235                 240

Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Gly Gly Gly
                245                 250                 255
```

Ser

<210> 84
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 84
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtctgcc atgccttgtg ctcccccgag 540

ggctgctggg gcccggagcc cagggactgc gtctctggtg gcggtggctc gggcggtggt 600

gggtcgggtg gcggcggatc tggtggcggt ggctcgctct gctacctgct ggatggaatc 660

ctcttcatct atggtgtcat tctcactgcc ttgttcctgg gaggtggaag c 711

<210> 85
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 85
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1   5   10   15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
            20   25   30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
        35   40   45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
    50   55   60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65   70   75   80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
                85   90   95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100   105   110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115   120   125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130   135   140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145   150   155   160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165   170   175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180   185   190

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
195 200 205

Gly Gly Gly Ser Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr
210 215 220

Gly Val Ile Leu Thr Ala Leu Phe Leu Gly Gly Gly Ser
225 230 235

<210> 86
<211> 1077
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 86
atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacacccagc attcctcctg 60

atcccacgca aagtgtgtaa cggaataggt attggtgaat ttaaagactc actctccata 120

aatgctacga atattaaaca cttcaaaaac tgcacctcca tcagtggcga tctccacatc 180

ctgccggtgg catttagggg tgactccttc acacatactc ctcctctgga tccacaggaa 240

ctggatattc tgaaaaccgt aaaggaaatc acagggtttt tgctgattca ggcttggcct 300

gaaaacagga cggacctcca tgcctttgag aacctagaaa tcatacgcgg caggaccaag 360

caacatggtc agttttctct tgcagtcgtc agcctgaaca taacatcctt gggattacgc 420

tccctcaagg agataagtga tggagatgtg ataatttcag gaaacaaaaa tttgtgctat 480

gcaaatacaa taaactggaa aaaactgttt gggacctccg gtcagaaaac caaaattata 540

agcaacagag gtgaaaacag ctgcaaggcc acaggccagg cctgccacca gctgtgcgcc 600

cgagggcact gctggggtcc agggcccacc cagtgtgtca actgcagcca gttccttcgg 660

ggccaggagt gcgtggagga atgccgagta ctgcaggggc tccccaggga gtatgtgaat 720

gccaggcact gtttgccgtg ccaccctgag tgtcagcccc agaatggctc agtgacctgt 780

tttggaccgg aggctgacca gtgtgtggcc tgtgcccact ataaggaccc tcccttctgc 840

gtggcccgct gccccagcgg tgtgaaacct gacctctcct acatgcccat ctggaagttt 900

ccagatgagg agggcgcatg ccagccttgc cccatcaact gcacccactc ctgtgtggac 960

ctggatgaca agggctgccc cgccgagcag agagccagcc ctctgacgtc catcatctct 1020

gcggtggttg gcattctgct ggtcgtggtc ttgggggtgg tctttgggat cctcatc 1077

<210> 87
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 87
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
20 25 30

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
35 40 45

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
50 55 60

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
65 70 75 80

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
85 90 95

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
100 105 110

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala

```
        115                 120                 125

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
    130                 135                 140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145                 150                 155                 160

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
                165                 170                 175

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
            180                 185                 190

Gln Ala Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly
        195                 200                 205

Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys
    210                 215                 220

Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn
225                 230                 235                 240

Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly
                245                 250                 255

Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala
            260                 265                 270

His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val
        275                 280                 285

Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu
    290                 295                 300

Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp
305                 310                 315                 320
```

Leu Asp Asp Lys Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr
325 330 335

Ser Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly
340 345 350

Val Val Phe Gly Ile Leu Ile
355

<210> 88
<211> 1011
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 88
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggcctgcc accagctgtg cgcccgaggg 540

cactgctggg gtccagggcc cacccagtgt gtcaactgca gccagttcct tcggggccag 600

gagtgcgtgg aggaatgccg agtactgcag gggctcccca gggagtatgt gaatgccagg 660

cactgtttgc cgtgccaccc tgagtgtcag ccccagaatg gctcagtgac ctgttttgga 720

ccggaggctg accagtgtgt ggcctgtgcc cactataagg accctccctt ctgcgtggcc 780

cgctgcccca gcggtgtgaa acctgacctc tcctacatgc ccatctggaa gtttccagat 840

gaggagggcg catgccagcc ttgccccatc aactgcaccc actcctgtgt ggacctggat 900

gacaagggct gccccgccga gcagagagcc agccctctga cgtccatcat ctctgcggtg 960

gttggcattc tgctggtcgt ggtcttgggg gtggtctttg ggatcctcat c 1011

<210> 89
<211> 337
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 89
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val

```
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Ala Cys His Gln Leu
                165                 170                 175

Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn
            180                 185                 190

Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val
        195                 200                 205

Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys Leu Pro
    210                 215                 220

Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly
225                 230                 235                 240

Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro
                245                 250                 255

Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr
            260                 265                 270

Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys
        275                 280                 285

Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly Cys
    290                 295                 300

Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser Ala Val
305                 310                 315                 320
```

Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly Ile Leu
325 330 335

Ile

<210> 90
<211> 1029
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 90
atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacacccagc attcctcctg 60

atcccacgca aagtgtgtaa cggaataggt attggtgaat ttaaagactc actctccata 120

aatgctacga atattaaaca cttcaaaaac tgcacctcca tcagtggcga tctccacatc 180

ctgccggtgg catttagggg tgactccttc acacatactc ctcctctgga tccacaggaa 240

ctggatattc tgaaaaccgt aaaggaaatc acagggtttt tgctgattca ggcttggcct 300

gaaaacagga cggacctcca tgcctttgag aacctagaaa tcatacgcgg caggaccaag 360

caacatggtc agttttctct tgcagtcgtc agcctgaaca taacatcctt gggattacgc 420

tccctcaagg agataagtga tggagatgtg ataatttcag gaaacaaaaa tttgtgctat 480

gcaaatacaa taaactggaa aaaactgttt gggacctccg gtcagaaaac caaaattata 540

agcaacagag gtgaaaacag ctgcaaggcc acaggccagg cctgccacca gctgtgcgcc 600

cgagggcact gctggggtcc agggcccacc cagtgtgtca actgcagcca gttccttcgg 660

ggccaggagt gcgtggagga atgccgagta ctgcaggggc tccccaggga gtatgtgaat 720

gccaggcact gtttgccgtg ccaccctgag tgtcagcccc agaatggctc agtgacctgt 780

tttggaccgg aggctgacca gtgtgtggcc tgtgcccact ataaggaccc tcccttctgc 840

gtggcccgct gccccagcgg tgtgaaacct gacctctcct acatgcccat ctggaagttt 900

ccagatgagg agggcgcatg ccagccttgc cccatcaact gcacccactc ccctctgacg 960

tccatcatct ctgcggtggt tggcattctg ctggtcgtgg tcttgggggt ggtctttggg 1020

atcctcatc 1029

<210> 91
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 91
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
20 25 30

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
35 40 45

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
50 55 60

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
65 70 75 80

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
85 90 95

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
100 105 110

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
115 120 125

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Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
    130                 135                 140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145                 150                 155                 160

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
                165                 170                 175

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
            180                 185                 190

Gln Ala Cys His Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly
        195                 200                 205

Pro Thr Gln Cys Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys
    210                 215                 220

Val Glu Glu Cys Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn
225                 230                 235                 240

Ala Arg His Cys Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly
                245                 250                 255

Ser Val Thr Cys Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala
            260                 265                 270

His Tyr Lys Asp Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val
        275                 280                 285

Lys Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu
    290                 295                 300

Gly Ala Cys Gln Pro Cys Pro Ile Asn Cys Thr His Ser Pro Leu Thr
305                 310                 315                 320
```

Ser Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly
325 330 335

Val Val Phe Gly Ile Leu Ile
340

<210> 92
<211> 963
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 92
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggcctgcc accagctgtg cgcccgaggg 540

cactgctggg gtccagggcc cacccagtgt gtcaactgca gccagttcct tcggggccag 600

gagtgcgtgg aggaatgccg agtactgcag gggctcccca gggagtatgt gaatgccagg 660

cactgtttgc cgtgccaccc tgagtgtcag ccccagaatg gctcagtgac ctgttttgga 720

ccggaggctg accagtgtgt ggcctgtgcc cactataagg accctccctt ctgcgtggcc 780

cgctgcccca gcggtgtgaa acctgacctc tcctacatgc ccatctggaa gtttccagat 840

gaggagggcg catgccagcc ttgccccatc aactgcaccc actcccctct gacgtccatc 900

atctctgcgg tggttggcat tctgctggtc gtggtcttgg gggtggtctt tgggatcctc 960

atc 963

<210> 93
<211> 321
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 93
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

```
Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Ala Cys His Gln Leu
                165                 170                 175

Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys Val Asn
            180                 185                 190

Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys Arg Val
        195                 200                 205

Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys Leu Pro
    210                 215                 220

Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys Phe Gly
225                 230                 235                 240

Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp Pro Pro
                245                 250                 255

Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu Ser Tyr
            260                 265                 270

Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Ala Cys Gln Pro Cys
        275                 280                 285

Pro Ile Asn Cys Thr His Ser Pro Leu Thr Ser Ile Ile Ser Ala Val
    290                 295                 300

Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly Ile Leu
305                 310                 315                 320

Ile
```

<210> 94
<211> 1080
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 94
atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacacccagc attcctcctg 60

atcccacgca aagtgtgtaa cggaataggt attggtgaat ttaaagactc actctccata 120

aatgctacga atattaaaca cttcaaaaac tgcacctcca tcagtggcga tctccacatc 180

ctgccggtgg catttagggg tgactccttc acacatactc ctcctctgga tccacaggaa 240

ctggatattc tgaaaaccgt aaaggaaatc acagggtttt tgctgattca ggcttggcct 300

gaaaacagga cggacctcca tgcctttgag aacctagaaa tcatacgcgg caggaccaag 360

caacatggtc agttttctct tgcagtcgtc agcctgaaca taacatcctt gggattacgc 420

tccctcaagg agataagtga tggagatgtg ataatttcag gaaacaaaaa tttgtgctat 480

gcaaatacaa taaactggaa aaaactgttt gggacctccg gtcagaaaac caaaattata 540

agcaacagag gtgaaaacag ctgcaaggcc acaggccagg tgtgtgaccc actgtgctcc 600

tctgggggat gctggggccc aggccctggt cagtgcttgt cctgtcgaaa ttatagccga 660

ggaggtgtct gtgtgaccca ctgcaacttt ctgaatgggg agcctcgaga atttgcccat 720

gaggccgaat gcttctcctg ccacccggaa tgccaaccca tggagggcac tgccacatgc 780

aatggctcgg gctctgatac ttgtgctcaa tgtgcccatt ttcgagatgg gccccactgt 840

gtgagcagct gcccccatgg agtcctaggt gccaagggcc caatctacaa gtacccagat 900

gttcagaatg aatgtcggcc ctgccatgag aactgcaccc aggggtgtaa aggaccagag 960

cttcaagact gtttaggaca aacactggtg ctgatcggca aaacccatct gacaatggct 1020

ttgacagtga tagcaggatt ggtagtgatt ttcatgatgc tgggcggcac ttttctctac 1080

<210> 95
<211> 360

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 95
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
20 25 30

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
35 40 45

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
50 55 60

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
65 70 75 80

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
85 90 95

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
100 105 110

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
115 120 125

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
130 135 140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145 150 155 160

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys

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                165                 170                 175

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
            180                 185                 190

Gln Val Cys Asp Pro Leu Cys Ser Ser Gly Gly Cys Trp Gly Pro Gly
        195                 200                 205

Pro Gly Gln Cys Leu Ser Cys Arg Asn Tyr Ser Arg Gly Gly Val Cys
    210                 215                 220

Val Thr His Cys Asn Phe Leu Asn Gly Glu Pro Arg Glu Phe Ala His
225                 230                 235                 240

Glu Ala Glu Cys Phe Ser Cys His Pro Glu Cys Gln Pro Met Glu Gly
                245                 250                 255

Thr Ala Thr Cys Asn Gly Ser Gly Ser Asp Thr Cys Ala Gln Cys Ala
            260                 265                 270

His Phe Arg Asp Gly Pro His Cys Val Ser Ser Cys Pro His Gly Val
        275                 280                 285

Leu Gly Ala Lys Gly Pro Ile Tyr Lys Tyr Pro Asp Val Gln Asn Glu
    290                 295                 300

Cys Arg Pro Cys His Glu Asn Cys Thr Gln Gly Cys Lys Gly Pro Glu
305                 310                 315                 320

Leu Gln Asp Cys Leu Gly Gln Thr Leu Val Leu Ile Gly Lys Thr His
                325                 330                 335

Leu Thr Met Ala Leu Thr Val Ile Ala Gly Leu Val Val Ile Phe Met
            340                 345                 350

Met Leu Gly Gly Thr Phe Leu Tyr
        355                 360
```

<210> 96
<211> 1014
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 96
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtgtgtg acccactgtg ctcctctggg 540

ggatgctggg gcccaggccc tggtcagtgc ttgtcctgtc gaaattatag ccgaggaggt 600

gtctgtgtga cccactgcaa ctttctgaat ggggagcctc gagaatttgc ccatgaggcc 660

gaatgcttct cctgccaccc ggaatgccaa cccatggagg gcactgccac atgcaatggc 720

tcgggctctg atacttgtgc tcaatgtgcc cattttcgag atgggcccca ctgtgtgagc 780

agctgccccc atggagtcct aggtgccaag ggcccaatct acaagtaccc agatgttcag 840

aatgaatgtc ggccctgcca tgagaactgc acccaggggt gtaaaggacc agagcttcaa 900

gactgtttag gacaaacact ggtgctgatc ggcaaaaccc atctgacaat ggctttgaca 960

gtgatagcag gattggtagt gattttcatg atgctgggcg gcacttttct ctac 1014

<210> 97
<211> 338

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 97
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys Asp Pro Leu

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                165                 170                 175

Cys Ser Ser Gly Gly Cys Trp Gly Pro Gly Pro Gly Gln Cys Leu Ser
            180                 185                 190

Cys Arg Asn Tyr Ser Arg Gly Gly Val Cys Val Thr His Cys Asn Phe
        195                 200                 205

Leu Asn Gly Glu Pro Arg Glu Phe Ala His Glu Ala Glu Cys Phe Ser
    210                 215                 220

Cys His Pro Glu Cys Gln Pro Met Glu Gly Thr Ala Thr Cys Asn Gly
225                 230                 235                 240

Ser Gly Ser Asp Thr Cys Ala Gln Cys Ala His Phe Arg Asp Gly Pro
                245                 250                 255

His Cys Val Ser Ser Cys Pro His Gly Val Leu Gly Ala Lys Gly Pro
            260                 265                 270

Ile Tyr Lys Tyr Pro Asp Val Gln Asn Glu Cys Arg Pro Cys His Glu
        275                 280                 285

Asn Cys Thr Gln Gly Cys Lys Gly Pro Glu Leu Gln Asp Cys Leu Gly
    290                 295                 300

Gln Thr Leu Val Leu Ile Gly Lys Thr His Leu Thr Met Ala Leu Thr
305                 310                 315                 320

Val Ile Ala Gly Leu Val Val Ile Phe Met Met Leu Gly Gly Thr Phe
                325                 330                 335

Leu Tyr
```

<210> 98
<211> 1101

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 98
atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacacccagc attcctcctg 60

atcccacgca aagtgtgtaa cggaataggt attggtgaat ttaaagactc actctccata 120

aatgctacga atattaaaca cttcaaaaac tgcacctcca tcagtggcga tctccacatc 180

ctgccggtgg catttagggg tgactccttc acacatactc ctcctctgga tccacaggaa 240

ctggatattc tgaaaaccgt aaaggaaatc acagggtttt tgctgattca ggcttggcct 300

gaaaacagga cggacctcca tgcctttgag aacctagaaa tcatacgcgg caggaccaag 360

caacatggtc agttttctct tgcagtcgtc agcctgaaca taacatcctt gggattacgc 420

tccctcaagg agataagtga tggagatgtg ataatttcag gaaacaaaaa tttgtgctat 480

gcaaatacaa taaactggaa aaaactgttt gggacctccg gtcagaaaac caaaattata 540

agcaacagag gtgaaaacag ctgcaaggcc acaggccagg tgtgcaacca tctgtgttcc 600

agtgatggct gttggggacc tgggccagac caatgtctgt cgtgtcgccg cttcagtaga 660

ggaaggatct gcatagagtc ttgtaacctc tatgatggtg aatttcggga gtttgagaat 720

ggctccatct gtgtggagtg tgacccccag tgtgagaaga tggaagatgg cctcctcaca 780

tgccatggac cgggtcctga caactgtaca aagtgctctc attttaaaga tggcccaaac 840

tgtgtggaaa aatgtccaga tggcttacag ggggcaaaca gtttcatttt caagtatgct 900

gatccagatc gggagtgcca cccatgccat ccaaactgca cccaagggtg taacggtccc 960

actagtcatg actgcattta ctacccatgg acgggccatt ccactttacc acaacatgct 1020

agaactcccc tgattgcagc tggagtaatt ggtgggctct tcattctggt cattgtgggt 1080

ctgacatttg ctgtttatgt t 1101

<210> 99
<211> 367

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 99
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
20 25 30

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
35 40 45

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
50 55 60

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
65 70 75 80

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
85 90 95

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
100 105 110

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
115 120 125

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
130 135 140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145 150 155 160

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys

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                165                 170                 175

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
            180                 185                 190

Gln Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys Trp Gly Pro Gly
        195                 200                 205

Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg Gly Arg Ile Cys
    210                 215                 220

Ile Glu Ser Cys Asn Leu Tyr Asp Gly Glu Phe Arg Glu Phe Glu Asn
225                 230                 235                 240

Gly Ser Ile Cys Val Glu Cys Asp Pro Gln Cys Glu Lys Met Glu Asp
                245                 250                 255

Gly Leu Leu Thr Cys His Gly Pro Gly Pro Asp Asn Cys Thr Lys Cys
            260                 265                 270

Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu Lys Cys Pro Asp Gly
        275                 280                 285

Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr Ala Asp Pro Asp Arg
    290                 295                 300

Glu Cys His Pro Cys His Pro Asn Cys Thr Gln Gly Cys Asn Gly Pro
305                 310                 315                 320

Thr Ser His Asp Cys Ile Tyr Tyr Pro Trp Thr Gly His Ser Thr Leu
                325                 330                 335

Pro Gln His Ala Arg Thr Pro Leu Ile Ala Ala Gly Val Ile Gly Gly
            340                 345                 350

Leu Phe Ile Leu Val Ile Val Gly Leu Thr Phe Ala Val Tyr Val
        355                 360                 365
```

<210> 100
<211> 1035
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 100
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtgtgca accatctgtg ttccagtgat 540

ggctgttggg gacctgggcc agaccaatgt ctgtcgtgtc gccgcttcag tagaggaagg 600

atctgcatag agtcttgtaa cctctatgat ggtgaatttc gggagtttga gaatggctcc 660

atctgtgtgg agtgtgaccc ccagtgtgag aagatggaag atggcctcct cacatgccat 720

ggaccgggtc ctgacaactg tacaaagtgc tctcatttta aagatggccc aaactgtgtg 780

gaaaaatgtc cagatggctt acaggggga aacagtttca ttttcaagta tgctgatcca 840

gatcgggagt gccacccatg ccatccaaac tgcacccaag ggtgtaacgg tcccactagt 900

catgactgca tttactaccc atggacgggc cattccactt taccacaaca tgctagaact 960

cccctgattg cagctggagt aattggtggg ctcttcattc tggtcattgt gggtctgaca 1020

tttgctgttt atgtt 1035

<210> 101
<211> 345
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 101
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

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Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys Asn His Leu
                165                 170                 175

Cys Ser Ser Asp Gly Cys Trp Gly Pro Gly Pro Asp Gln Cys Leu Ser
            180                 185                 190

Cys Arg Arg Phe Ser Arg Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu
        195                 200                 205

Tyr Asp Gly Glu Phe Arg Glu Phe Glu Asn Gly Ser Ile Cys Val Glu
    210                 215                 220

Cys Asp Pro Gln Cys Glu Lys Met Glu Asp Gly Leu Leu Thr Cys His
225                 230                 235                 240

Gly Pro Gly Pro Asp Asn Cys Thr Lys Cys Ser His Phe Lys Asp Gly
                245                 250                 255

Pro Asn Cys Val Glu Lys Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser
            260                 265                 270

Phe Ile Phe Lys Tyr Ala Asp Pro Asp Arg Glu Cys His Pro Cys His
        275                 280                 285

Pro Asn Cys Thr Gln Gly Cys Asn Gly Pro Thr Ser His Asp Cys Ile
    290                 295                 300

Tyr Tyr Pro Trp Thr Gly His Ser Thr Leu Pro Gln His Ala Arg Thr
305                 310                 315                 320

Pro Leu Ile Ala Ala Gly Val Ile Gly Gly Leu Phe Ile Leu Val Ile
                325                 330                 335

Val Gly Leu Thr Phe Ala Val Tyr Val
            340                 345
```

<210> 102
<211> 1071
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 102
atgcttctcc tggtgacaag ccttctgctc tgtgagttac cacacccagc attcctcctg 60

atcccacgca aagtgtgtaa cggaataggt attggtgaat ttaaagactc actctccata 120

aatgctacga atattaaaca cttcaaaaac tgcacctcca tcagtggcga tctccacatc 180

ctgccggtgg catttagggg tgactccttc acacatactc ctcctctgga tccacaggaa 240

ctggatattc tgaaaaccgt aaaggaaatc acagggtttt tgctgattca ggcttggcct 300

gaaaacagga cggacctcca tgcctttgag aacctagaaa tcatacgcgg caggaccaag 360

caacatggtc agttttctct tgcagtcgtc agcctgaaca taacatcctt gggattacgc 420

tccctcaagg agataagtga tggagatgtg ataatttcag gaaacaaaaa tttgtgctat 480

gcaaatacaa taaactggaa aaaactgttt gggacctccg gtcagaaaac caaaattata 540

agcaacagag gtgaaaacag ctgcaaggcc acaggccagg tgtgcaacca tctgtgttcc 600

agtgatggct gttggggacc tgggccagac caatgtctgt cgtgtcgccg cttcagtaga 660

ggaaggatct gcatagagtc ttgtaacctc tatgatggtg aatttcggga gtttgagaat 720

ggctccatct gtgtggagtg tgacccccag tgtgagaaga tggaagatgg cctcctcaca 780

tgccatggac cgggtcctga caactgtaca aagtgctctc attttaaaga tggcccaaac 840

tgtgtggaaa aatgtccaga tggcttacag ggggcaaaca gtttcatttt caagtatgct 900

gatccagatc gggagtgcca cccatgccat ccaaactgca cccaagggtg cataggctca 960

agtattgaag actgcatcgg cctgatggat agaactcccc tgattgcagc tggagtaatt 1020

ggtgggctct tcattctggt cattgtgggt ctgacatttg ctgtttatgt t 1071

<210> 103
<211> 357

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 103
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
20 25 30

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
35 40 45

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
50 55 60

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
65 70 75 80

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
85 90 95

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
100 105 110

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
115 120 125

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
130 135 140

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
145 150 155 160

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys

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                165                 170                 175

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
            180                 185                 190

Gln Val Cys Asn His Leu Cys Ser Ser Asp Gly Cys Trp Gly Pro Gly
        195                 200                 205

Pro Asp Gln Cys Leu Ser Cys Arg Arg Phe Ser Arg Gly Arg Ile Cys
    210                 215                 220

Ile Glu Ser Cys Asn Leu Tyr Asp Gly Glu Phe Arg Glu Phe Glu Asn
225                 230                 235                 240

Gly Ser Ile Cys Val Glu Cys Asp Pro Gln Cys Glu Lys Met Glu Asp
                245                 250                 255

Gly Leu Leu Thr Cys His Gly Pro Gly Pro Asp Asn Cys Thr Lys Cys
            260                 265                 270

Ser His Phe Lys Asp Gly Pro Asn Cys Val Glu Lys Cys Pro Asp Gly
        275                 280                 285

Leu Gln Gly Ala Asn Ser Phe Ile Phe Lys Tyr Ala Asp Pro Asp Arg
    290                 295                 300

Glu Cys His Pro Cys His Pro Asn Cys Thr Gln Gly Cys Ile Gly Ser
305                 310                 315                 320

Ser Ile Glu Asp Cys Ile Gly Leu Met Asp Arg Thr Pro Leu Ile Ala
                325                 330                 335

Ala Gly Val Ile Gly Gly Leu Phe Ile Leu Val Ile Val Gly Leu Thr
            340                 345                 350

Phe Ala Val Tyr Val
        355
```

<210> 104
<211> 1005
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 104
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc caggtgtgca accatctgtg ttccagtgat 540

ggctgttggg gacctgggcc agaccaatgt ctgtcgtgtc gccgcttcag tagaggaagg 600

atctgcatag agtcttgtaa cctctatgat ggtgaatttc gggagtttga gaatggctcc 660

atctgtgtgg agtgtgaccc ccagtgtgag aagatggaag atggcctcct cacatgccat 720

ggaccgggtc ctgacaactg tacaaagtgc tctcatttta aagatggccc aaactgtgtg 780

gaaaaatgtc cagatggctt acaggggga aacagtttca ttttcaagta tgctgatcca 840

gatcgggagt gccacccatg ccatccaaac tgcacccaag ggtgcatagg ctcaagtatt 900

gaagactgca tcggcctgat ggatagaact cccctgattg cagctggagt aattggtggg 960

ctcttcattc tggtcattgt gggtctgaca tttgctgttt atgtt 1005

<210> 105
<211> 335

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 105
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys Asn His Leu

```
                165                 170                 175

Cys Ser Ser Asp Gly Cys Trp Gly Pro Gly Pro Asp Gln Cys Leu Ser
            180                 185                 190

Cys Arg Arg Phe Ser Arg Gly Arg Ile Cys Ile Glu Ser Cys Asn Leu
        195                 200                 205

Tyr Asp Gly Glu Phe Arg Glu Phe Glu Asn Gly Ser Ile Cys Val Glu
    210                 215                 220

Cys Asp Pro Gln Cys Glu Lys Met Glu Asp Gly Leu Leu Thr Cys His
225                 230                 235                 240

Gly Pro Gly Pro Asp Asn Cys Thr Lys Cys Ser His Phe Lys Asp Gly
                245                 250                 255

Pro Asn Cys Val Glu Lys Cys Pro Asp Gly Leu Gln Gly Ala Asn Ser
            260                 265                 270

Phe Ile Phe Lys Tyr Ala Asp Pro Asp Arg Glu Cys His Pro Cys His
        275                 280                 285

Pro Asn Cys Thr Gln Gly Cys Ile Gly Ser Ser Ile Glu Asp Cys Ile
    290                 295                 300

Gly Leu Met Asp Arg Thr Pro Leu Ile Ala Ala Gly Val Ile Gly Gly
305                 310                 315                 320

Leu Phe Ile Leu Val Ile Val Gly Leu Thr Phe Ala Val Tyr Val
                325                 330                 335
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<210> 106
<211> 891
<212> DNA
<213> Unknown

<220>

<223> Description of Unknown:
Full length CD20 sequence

<400> 106
atgacaacac ccagaaattc agtaaatggg actttcccgg cagagccaat gaaaggccct 60

attgctatgc aatctggtcc aaaaccactc ttcaggagga tgtcttcact ggtgggcccc 120

acgcaaagct tcttcatgag ggaatctaag actttggggg ctgtccagat tatgaatggg 180

ctcttccaca ttgccctggg gggtcttctg atgatcccag cagggatcta tgcacccatc 240

tgtgtgactg tgtggtaccc tctctgggga ggcattatgt atattatttc cggatcactc 300

ctggcagcaa cggagaaaaa ctccaggaag tgtttggtca aaggaaaaat gataatgaat 360

tcattgagcc tctttgctgc catttctgga atgattcttt caatcatgga catacttaat 420

attaaaattt cccatttttt aaaaatggag agtctgaatt ttattagagc tcacacacca 480

tatattaaca tatacaactg tgaaccagct aatccctctg agaaaaactc cccatctacc 540

caatactgtt acagcataca atctctgttc ttgggcattt tgtcagtgat gctgatcttt 600

gccttcttcc aggaacttgt aatagctggc atcgttgaga atgaatggaa aagaacgtgc 660

tccagaccca aatctaacat agttctcctg tcagcagaag aaaaaaaaga acagactatt 720

gaaataaaag aagaagtggt tgggctaact gaaacatctt cccaaccaaa gaatgaagaa 780

gacattgaaa ttattccaat ccaagaagag gaagaagaag aaacagagac gaactttcca 840

gaacctcccc aagatcagga atcctcacca atagaaaatg acagctctcc t 891

<210> 107
<211> 297
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Full length CD20 sequence

<400> 107
Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

```
Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
            20                  25                  30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
        35                  40                  45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
    50                  55                  60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65                  70                  75                  80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
                85                  90                  95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
            100                 105                 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
        115                 120                 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
    130                 135                 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145                 150                 155                 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
                165                 170                 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
            180                 185                 190

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
        195                 200                 205

Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
```

```
    210                 215                 220

Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225                 230                 235                 240

Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
                245                 250                 255

Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu
            260                 265                 270

Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser
        275                 280                 285

Ser Pro Ile Glu Asn Asp Ser Ser Pro
    290                 295
```

<210> 108
<211> 789
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 108
atgaccacac cacggaactc tgtgaatggc accttcccag cagagccaat gaagggacca 60

atcgcaatgc agagcggacc caagcctctg tttcggagaa tgagctccct ggtgggccca 120

acccagtcct tctttatgag agagtctaag acactgggcg ccgtgcagat catgaacgga 180

ctgttccaca tcgccctggg aggactgctg atgatcccag ccggcatcta cgcccctatc 240

tgcgtgaccg tgtggtaccc tctgtggggc ggcatcatgt atatcatctc cggctctctg 300

ctggccgcca cagagaagaa cagcaggaag tgtctggtga agggcaagat gatcatgaat 360

agcctgtccc tgtttgccgc catctctggc atgatcctga gcatcatgga catcctgaac 420

atcaagatca gccacttcct gaagatggag agcctgaact tcatcagagc ccacacccct 480

tacatcaaca tctataattg cgagcctgcc aacccatccg agaagaattc tccaagcaca 540

cagtactgtt attccatcca gtctctgttc ctgggcatcc tgtctgtgat gctgatcttt 600

gccttctttc aggagctggt catcgccggc atcgtggaga acgagtggaa gaggacctgc 660

agccgcccca agtccaatat cgtgctgctg tccgccgagg agaagaagga gcagacaatc 720

gagatcaagg aggaggtggt gggcctgacc gagacatcta gccagcctaa gaatgaggag 780

gatatcgag 789

<210> 109
<211> 263
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 109
Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
50 55 60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65 70 75 80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
85 90 95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
100 105 110

```
Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
        115                 120                 125


Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
    130                 135                 140


His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145                 150                 155                 160


Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
                165                 170                 175


Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
            180                 185                 190


Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
        195                 200                 205


Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys
    210                 215                 220


Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile
225                 230                 235                 240


Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser Gln Pro
                245                 250                 255


Lys Asn Glu Glu Asp Ile Glu
            260
```

<210> 110
<211> 294
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polynucleotide

<400> 110
atgataatga attcattgag cctctttgct gccatttctg gaatgattct ttcaatcatg 60

gacatactta atattaaaat ttcccatttt ttaaaaatgg agagtctgaa ttttattaga 120

gctcacacac catatattaa catatacaac tgtgaaccag ctaatccctc tgagaaaaac 180

tccccatcta cccaatactg ttacagcata caatctctgt tcttgggcat tttgtcagtg 240

atgctgatct ttgccttctt ccaggaactt gtaatagctg gcatcgttga gaat 294

<210> 111
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 111
Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile
1 5 10 15

Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys
20 25 30

Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile
35 40 45

Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr
50 55 60

Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val
65 70 75 80

Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val
85 90 95

Glu Asn

<210> 112
<211> 267
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 112
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgaaaattt cccatttttt aaaaatggag agtctgaatt ttattagagc tcacacacca 120

tatattaaca tatacaactg tgaaccagct aatccctctg agaaaaactc cccatctacc 180

caatactgtt acagcataca atctatctac atctgggcgc ccttggccgg gacttgtggg 240

gtccttctcc tgtcactggt tatcacc 267

<210> 113
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 113
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu
20 25 30

Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu
35 40 45

Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr
50 55 60

Ser Ile Gln Ser Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
65 70 75 80

Val Leu Leu Leu Ser Leu Val Ile Thr
85

<210> 114
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 114
atgacaacac ccagaaattc agtaaatggg actttcccgg cagagccaat gaaaggccct 60

attgctatgc aatctggtcc aaaaccactc ttcaggagga tgtcttcact ggtgggcccc 120

acgcaaagct tcttcatgag ggaatctaag actttggggg ctgtccagat tatgaatggg 180

ctcttccaca ttgccctggg gggtcttctg atgatcccag cagggatcta tgcacccatc 240

tgtgtgactg tgtggtaccc tctctgggga ggcattatgt atattatttc cggatcactc 300

ctggcagcaa cggagaaaaa ctccaggaag tgtttggtca aaggaaaaat gataatgaat 360

tcattgagcc tctttgctgc catttctgga atgattcttt caatcatgga catacttaat 420

attaaaattt cccatttttt aaaaatggag agtctgaatt ttattagagc tcacacacca 480

tatattaaca tatacaactg tgaaccagct aatccctctg agaaaaactc cccatctacc 540

caatactgtt acagcataca atctctgttc ttgggcattt tgtcagtgat gctgatcttt 600

gccttcttcc aggaacttgt aatagctggc atcgttgaga at 642

<210> 115
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 115

```
Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1               5                  10                  15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
            20                  25                  30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
        35                  40                  45

Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe His Ile
    50                  55                  60

Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala Pro Ile
65                  70                  75                  80

Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile
                85                  90                  95

Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu
            100                 105                 110

Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile
        115                 120                 125

Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser
    130                 135                 140

His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro
145                 150                 155                 160

Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn
                165                 170                 175

Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly
            180                 185                 190
```

Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile
195 200 205

Ala Gly Ile Val Glu Asn
210

<210> 116
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 116
gtgactgtgt ggtaccctct ctggggaggc attatgtata ttatttccgg atcactcctg 60

gcagcaacgg agaaaaactc caggaagtgt ttggtcaaag gaaaaatgat aatgaattca 120

ttgagcctct ttgctgccat ttctggaatg attctttcaa tcatggacat acttaatatt 180

aaaatttccc atttttaaa aatggagagt ctgaatttta ttagagctca cacaccatat 240

attaacatat acaactgtga accagctaat ccctctgaga aaaactcccc atctacccaa 300

tactgttaca gcatacaatc tctgttcttg ggcattttgt cagtgatgct gatctttgcc 360

ttcttccagg aacttgtaat agctggcatc gttgagaat 399

<210> 117
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 117
Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile Ser
1 5 10 15

Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu Val
            20   25   30

Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser
        35   40   45

Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser His
    50   55   60

Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr
65   70   75   80

Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser
                85   90   95

Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile
            100   105   110

Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala
        115   120   125

Gly Ile Val Glu Asn
    130

<210> 118
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 118
gtgactgtgt ggtaccctct ctggggaggc attatgtata ttatttccgg atcactcctg 60

gcagcaacgg agaaaaactc caggaagtgt ttggtcaaag gaaaaatgat aatgaattca 120

ttgagcctct ttgctgccat ttctggaatg attctttcaa tcatggacat acttaatatt 180

aaaatttccc atttttaaa aatggagagt ctgaatttta ttagagctca cacaccatat 240

attaacatat acaactgtga accagctaat ccctctgaga aaaactcccc atctacccaa 300

tactgttaca gcata 315

<210> 119
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 119
Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr Ile Ile Ser
1 5 10 15

Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys Cys Leu Val
20 25 30

Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser
35 40 45

Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys Ile Ser His
50 55 60

Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr
65 70 75 80

Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser
85 90 95

Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile
100 105 110

Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala
115 120 125

Gly Ile Val Glu Asn

130

<210> 120
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 120
ccatatatta acatatacaa ctgtgaacca gctaatccct ctgagaaaaa ctccccatct 60

acccaatact gttacagcat acaatcgggt ggcggcggat ctattgaagt tatgtatcct 120

cctccttacc tagacaatga gaagagcaat ggaaccatta tccatgtgaa agggaaacac 180

ctttgtccaa gtcccctatt tcccggacct tctaagccct tttgggtgct ggtggtggtt 240

ggtggagtcc tggcttgcta tagcttgcta gtaacagtgg cctttattat tttctgggtg 300

aggagtaaga ggagcaggct cctgcacagt gac 333

<210> 121
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 121
Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys
1 5 10 15

Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Gly Gly Gly
20 25 30

Gly Ser Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys
35 40 45

Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser

50 55 60

Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val
65 70 75 80

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
85 90 95

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
100 105 110

<210> 122
<211> 435
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 122
ccatatatta acatatacaa ctgtgaacca gctaatccct ctgagaaaaa ctccccatct 60

acccaatact gttacagcat acaatcgggt ggcggcggat ctccatatat taacatatac 120

aactgtgaac cagctaatcc ctctgagaaa aactccccat ctacccaata ctgttacagc 180

atacaatcgg gtggcggcgg atctattgaa gttatgtatc ctcctcctta cctagacaat 240

gagaagagca atggaaccat tatccatgtg aaagggaaac acctttgtcc aagtccccta 300

tttcccggac cttctaagcc cttttgggtg ctggtggtgg ttggtggagt cctggcttgc 360

tatagcttgc tagtaacagt ggcctttatt attttctggg tgaggagtaa gaggagcagg 420

ctcctgcaca gtgac 435

<210> 123
<211> 145
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 123
Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys
1 5 10 15

Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Gly Gly Gly
20 25 30

Gly Ser Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser
35 40 45

Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Gly
50 55 60

Gly Gly Gly Ser Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn
65 70 75 80

Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys
85 90 95

Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val
100 105 110

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
115 120 125

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
130 135 140

Asp
145

<210> 124
<211> 348
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 124
ccatatatta acatatacaa ctgtgaacca gctaatccct ctgagaaaaa ctccccatct 60

acccaatact gttacagcat acaatcgggt ggcggcggat ctccagcgcc gcgaccacca 120

acaccggcgc ccaccatcgc gtcgcagccc ctgtccctgc gcccagaggc gtgccggcca 180

gcggcggggg gcgcagtgca cacgaggggg ctggacttcg cctgtgatat ctacatctgg 240

gcgcccttgg ccgggacttg tggggtcctt ctcctgtcac tggttatcac cctttactgc 300

aaccacagga accgaagacg tgtttgcaaa tgtccccggc ctgtggtc 348

<210> 125
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 125
Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys
1 5 10 15

Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Gly Gly Gly
20 25 30

Gly Ser Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
35 40 45

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
50 55 60

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
65 70 75 80

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
85 90 95

Thr Leu Tyr Cys Asn His Arg Asn Arg Arg Arg Val Cys Lys Cys Pro
100 105 110

Arg Pro Val Val
115

<210> 126
<211> 300
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 126
tgtgaaccag ctaatccctc tgagaaaaac tccccatcta cccaatactg ttcgggtggc 60

ggcggatcta ttgaagttat gtatcctcct ccttacctag acaatgagaa gagcaatgga 120

accattatcc atgtgaaagg gaaacacctt tgtccaagtc ccctatttcc cggaccttct 180

aagccctttt gggtgctggt ggtggttggt ggagtcctgg cttgctatag cttgctagta 240

acagtggcct ttattatttt ctgggtgagg agtaagagga gcaggctcct gcacagtgac 300

<210> 127
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 127
Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr
1 5 10 15

Cys Ser Gly Gly Gly Gly Ser Ile Glu Val Met Tyr Pro Pro Pro Tyr
20 25 30

```
Leu Asp Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys
        35                  40                  45


His Leu Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp
    50                  55                  60


Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
65                  70                  75                  80


Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu
                85                  90                  95


Leu His Ser Asp
            100
```

<210> 128
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 128
tgtgaaccag ctaatccctc tgagaaaaac tccccatcta cccaatactg ttcgggtggc 60

ggcggatctt gtgaaccagc taatccctct gagaaaaact ccccatctac ccaatactgt 120

tcgggtggcg gcggatctat tgaagttatg tatcctcctc cttacctaga caatgagaag 180

agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc 240

ggaccttcta agccctttg ggtgctggtg gtggttggtg gagtcctggc ttgctatagc 300

ttgctagtaa cagtggcctt tattattttc tgggtgagga gtaagaggag caggctcctg 360

cacagtgac 369

<210> 129
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 129
Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr
1 5 10 15

Cys Ser Gly Gly Gly Gly Ser Cys Glu Pro Ala Asn Pro Ser Glu Lys
20 25 30

Asn Ser Pro Ser Thr Gln Tyr Cys Ser Gly Gly Gly Gly Ser Ile Glu
35 40 45

Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser Asn Gly Thr
50 55 60

Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro Leu Phe Pro
65 70 75 80

Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu
85 90 95

Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
100 105 110

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
115 120

<210> 130
<211> 315
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 130
tgtgaaccag ctaatccctc tgagaaaaac tccccatcta cccaatactg ttcgggtggc 60

ggcggatctc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 120

tccctgcgcc cagaggcgtg ccggccagcg gcgggggggcg cagtgcacac gagggggctg 180

gacttcgcct gtgatatcta catctgggcg cccttggccg ggacttgtgg ggtccttctc 240

ctgtcactgg ttatcaccct ttactgcaac cacaggaacc gaagacgtgt ttgcaaatgt 300

ccccggcctg tggtc 315

<210> 131
<211> 105
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 131
Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr
1 5 10 15

Cys Ser Gly Gly Gly Gly Ser Pro Ala Pro Arg Pro Pro Thr Pro Ala
20 25 30

Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg
35 40 45

Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys
50 55 60

Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu
65 70 75 80

Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn Arg Arg Arg
85 90 95

Val Cys Lys Cys Pro Arg Pro Val Val
100 105

<210> 132
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 132
atgaccacac cccggaactc cgtgaatggc accttccctg ccgagccaat gaagggccct 60

atcgccatgc agtctggccc aaagcccctg tttcggagaa tgagctccct ggtgggcccc 120

acccagagct tctttatgag ggagtccaag acactgggcg cctgcctggt gaagggcaag 180

atgatcatga actctctgag cctgttcgcc gccatctccg gcatgatcct gtctatcatg 240

gacatcctga acatcaagat ctctcacttc ctgaagatgg agagcctgaa cttcatccgg 300

gcccacaccc catacatcaa catctataat tgcgagcccg ccaaccctag cgagaagaat 360

tccccctcta cacagtactg ttatagcatc cagtccctgt tcctgggcat cctgtccgtg 420

atgctgatct ttgccttctt tcaggagctg gtcatcgccg gcatcgtgga gaacgagtgg 480

aagaggacct gttctcgccc taagagcaat atcgtgctgc tgagcgccga ggagaagaag 540

gagcagacaa tcgagatcaa ggaggaggtg gtgggcctga ccgagacatc tagccagcct 600

aagaatgagg aggatatcga gatcatccca atccaggagg aggaggagga ggagaccgag 660

acaaactttc cagagccccc tcaggaccag gagtcctctc caatcgagaa tgatagctcc 720

ccctgataa 729

<210> 133
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 133
Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro

```
1               5                   10                  15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
            20                  25                  30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
        35                  40                  45

Ser Lys Thr Leu Gly Ala Cys Leu Val Lys Gly Lys Met Ile Met Asn
    50                  55                  60

Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile Met
65                  70                  75                  80

Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu
                85                  90                  95

Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu
            100                 105                 110

Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr
        115                 120                 125

Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile Phe
    130                 135                 140

Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu Trp
145                 150                 155                 160

Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val Leu Leu Ser Ala
                165                 170                 175

Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val Gly
            180                 185                 190

Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu Ile
        195                 200                 205
```

Ile Pro Ile Gln Glu Glu Glu Glu Glu Thr Glu Thr Asn Phe Pro
210 215 220

Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile Glu Asn Asp Ser Ser
225 230 235 240

<210> 134
<211> 681
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 134
atgaccacac cacggaacag cgtgaatggc accttcccag cagagccaat gaagggacca 60

atcgcaatgc agtccggacc caagcctctg tttcggagaa tgagctccct ggtgggcccc 120

acccagtctt tctttatgag ggagagcaag acactgggcg cctgcctggt gaagggcaag 180

atgatcatga actccctgtc tctgttcgcc gccatcagcg gcatgatcct gtccatcatg 240

gacatcctga acatcaagat ctcccacttc ctgaagatgg agagcctgaa cttcatccgg 300

gcccacaccc cttacatcaa catctataat tgcgagcctg ccaacccatc tgagaagaat 360

agcccatcca cacagtactg ttattctatc cagagcctgt tcctgggcat cctgtccgtg 420

atgctgatct ttgccttctt tcaggagctg gtcatcgccg gcatcgtgga gaacgagtgg 480

aagaggacct gttcccgccc caagtctaat atcgtgctgc tgagcgccga ggagaagaag 540

gagcagacaa tcgagatcaa ggaggaggtg gtgggcctga ccgagacatc tagccagccc 600

aagaacgagg aggatatcga gatcatccct atccaggagg aggaggagga ggagaccgag 660

acaaattttc ctgagtgata a 681

<210> 135
<211> 225
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 135
Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Cys Leu Val Lys Gly Lys Met Ile Met Asn
50 55 60

Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile Met
65 70 75 80

Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu
85 90 95

Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu
100 105 110

Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr
115 120 125

Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile Phe
130 135 140

Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu Trp
145 150 155 160

Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val Leu Leu Ser Ala
165 170 175

Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val Gly
180 185 190

Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu Ile
195 200 205

Ile Pro Ile Gln Glu Glu Glu Glu Glu Glu Thr Glu Thr Asn Phe Pro
210 215 220

Glu
225

<210> 136
<211> 627
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 136
atgaccacac cccggaacag cgtgaatggc accttcccag ccgagcccat gaagggccct 60

atcgccatgc agtccggccc caagcctctg tttcggagaa tgagctccct ggtgggcccc 120

acccagtctt tctttatgag ggagagcaag acactgggcg cctgcctggt gaagggcaag 180

atgatcatga actccctgtc tctgttcgcc gccatcagcg gcatgatcct gtccatcatg 240

gacatcctga acatcaagat ctcccacttc ctgaagatgg agagcctgaa cttcatccgg 300

gcccacaccc catacatcaa catctataat tgcgagcctg ccaacccatc tgagaagaat 360

agcccctcca cacagtactg ttattctatc cagagcctgt tcctgggcat cctgtccgtg 420

atgctgatct ttgccttctt tcaggagctg gtcatcgccg gcatcgtgga gaacgagtgg 480

aagaggacct gttcccgccc taagtctaat atcgtgctgc tgagcgccga ggagaagaag 540

gagcagacaa tcgagatcaa ggaggaggtg gtgggcctga ccgagacatc tagccagcca 600

aagaatgagg aggatatcga gtgataa 627

<210> 137
<211> 207
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 137
Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1 5 10 15

Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
20 25 30

Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
35 40 45

Ser Lys Thr Leu Gly Ala Cys Leu Val Lys Gly Lys Met Ile Met Asn
50 55 60

Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile Met
65 70 75 80

Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu
85 90 95

Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu
100 105 110

Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr
115 120 125

Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile Phe
130 135 140

Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu Trp
145 150 155 160

Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val Leu Leu Ser Ala
165 170 175

Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val Val Gly
180 185 190

Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile Glu
195 200 205

<210> 138
<211> 522
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 138
atgaccacac cccggaactc cgtgaatggc accttcccag ccgagcccat gaagggccct 60

atcgccatgc agtctggccc caagcctctg tttcggagaa tgagctccct ggtgggccct 120

acccagagct tctttatgag ggagtccaag acactgggcg cctgcctggt gaagggcaag 180

atgatcatga actctctgag cctgttcgcc gccatctccg gcatgatcct gtctatcatg 240

gacatcctga acatcaagat ctctcacttc ctgaagatgg agagcctgaa cttcatccgg 300

gcccacaccc catacatcaa catctataat tgcgagcctg ccaacccaag cgagaagaat 360

tccccctcta cacagtactg ttatagcatc cagtccctgt tcctgggcat cctgtccgtg 420

atgctgatct ttgccttctt tcaggagctg gtcatcgccg gcatcgtgga gaacgagtgg 480

aagaggacat gttctcgccc caagagcaat atcgtgtgat aa 522

<210> 139
<211> 172
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 139

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Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala Glu Pro
1               5                   10                  15


Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu Phe Arg
            20                  25                  30


Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met Arg Glu
        35                  40                  45


Ser Lys Thr Leu Gly Ala Cys Leu Val Lys Gly Lys Met Ile Met Asn
    50                  55                  60


Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser Ile Met
65                  70                  75                  80


Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu
                85                  90                  95


Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu
            100                 105                 110


Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr
        115                 120                 125


Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu Ile Phe
    130                 135                 140


Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn Glu Trp
145                 150                 155                 160


Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val
                165                 170
```

<210> 140

<211> 591
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 140
atgaccacac ccaggaacag cgtgtgcctg gtgaagggca agatgatcat gaatagcctg 60

tccctgttcg ccgccatctc tggcatgatc ctgagcatca tggacatcct gaacatcaag 120

atctcccact tcctgaagat ggagagcctg aacttcatcc gggcccacac cccatacatc 180

aacatctata attgcgagcc agccaacccc agcgagaaga attctcccag cacacagtac 240

tgttattcca tccagtctct gttcctgggc atcctgtccg tgatgctgat ctttgccttc 300

tttcaggagc tggtcatcgc cggcatcgtg gagaacgagt ggaagcggac ctgtagcaga 360

cctaagtcca atatcgtgct gctgtccgcc gaggagaaga aggagcagac aatcgagatc 420

aaggaggagg tggtgggcct gaccgagaca agctcccagc ccaagaacga ggaggatatc 480

gagatcatcc ctatccagga ggaggaggag gaggagaccg agacaaactt tccagagccc 540

cctcaggacc aggagtctag ccctatcgag aatgattcct ctccatgata a 591

<210> 141
<211> 195
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 141
Met Thr Thr Pro Arg Asn Ser Val Cys Leu Val Lys Gly Lys Met Ile
1 5 10 15

Met Asn Ser Leu Ser Leu Phe Ala Ala Ile Ser Gly Met Ile Leu Ser
20 25 30

Ile Met Asp Ile Leu Asn Ile Lys Ile Ser His Phe Leu Lys Met Glu

35 40 45

Ser Leu Asn Phe Ile Arg Ala His Thr Pro Tyr Ile Asn Ile Tyr Asn
50 55 60

Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr
65 70 75 80

Cys Tyr Ser Ile Gln Ser Leu Phe Leu Gly Ile Leu Ser Val Met Leu
85 90 95

Ile Phe Ala Phe Phe Gln Glu Leu Val Ile Ala Gly Ile Val Glu Asn
100 105 110

Glu Trp Lys Arg Thr Cys Ser Arg Pro Lys Ser Asn Ile Val Leu Leu
115 120 125

Ser Ala Glu Glu Lys Lys Glu Gln Thr Ile Glu Ile Lys Glu Glu Val
130 135 140

Val Gly Leu Thr Glu Thr Ser Ser Gln Pro Lys Asn Glu Glu Asp Ile
145 150 155 160

Glu Ile Ile Pro Ile Gln Glu Glu Glu Glu Glu Glu Thr Glu Thr Asn
165 170 175

Phe Pro Glu Pro Pro Gln Asp Gln Glu Ser Ser Pro Ile Glu Asn Asp
180 185 190

Ser Ser Pro
195

<210> 142
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 142
ggacaaaacg acaccagcca aaccagcagc ccctca 36

<210> 143
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 143
Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
1 5 10

<210> 144
<211> 279
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 144
atgaagcgct tcctcttcct cctactcacc atcagcctcc tggttatggt acagatacaa 60

actggactct caggacaaaa cgacaccagc caaaccagca gcccctcagg cagcacctcc 120

ggcagcggca agcctggcag cggcgagggc agcaccaagg gcggcggagg cggaagcgga 180

ggcggaggct ccaagccctt ctgggtgctg gtcgtggtcg gcggagtgct ggcctgttac 240

agcctgctgg tcaccgtggc cttcatcatc ttttgggtc 279

<210> 145
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

polypeptide

<400> 145
Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
35 40 45

Glu Gly Ser Thr Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
50 55 60

Lys Pro Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
65 70 75 80

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
85 90

<210> 146
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 146
atgaagcgct tcctcttcct cctactcacc atcagcctcc tggttatggt acagatacaa 60

actggactct caggacaaaa cgacaccagc caaaccagca gcccctcagg cagcacctcc 120

ggcagcggca agcctggcag cggcgagggc agcaccaagg gcggccagaa tgatacatct 180

cagacttcat ctcctagcgg atccacttct ggttccggta aaccaggttc tggggaaggt 240

agtacaaaag gaggcggagg cggaagcgga ggcggaggct ccaagccctt ctgggtgctg 300

gtcgtggtcg gcggagtgct ggcctgttac agcctgctgg tcaccgtggc cttcatcatc 360

ttttgggtc 369

<210> 147
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 147
Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
35 40 45

Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
50 55 60

Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
65 70 75 80

Ser Thr Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Pro
85 90 95

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
100 105 110

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
115 120

<210> 148
<211> 459
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 148
atgaagcgct tcctcttcct cctactcacc atcagcctcc tggttatggt acagatacaa 60

actggactct caggacaaaa cgacaccagc caaaccagca gcccctcagg cagcacctcc 120

ggcagcggca agcctggcag cggcgagggc agcaccaagg gcggccagaa tgatacatct 180

cagacttcat ctcctagcgg atccacttct ggttccggta aaccaggttc tggggaaggt 240

agtacaaaag gaggtcagaa cgacacttca cagacatcta gtccatccgg cagtacaagc 300

ggaagtggaa agcccggaag tggtgaggga tcaactaagg gtggcggagg cggaagcgga 360

ggcggaggct ccaagccctt ctgggtgctg gtcgtggtcg gcggagtgct ggcctgttac 420

agcctgctgg tcaccgtggc cttcatcatc ttttgggtc 459

<210> 149
<211> 153
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 149
Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
35 40 45

Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
50 55 60

```
Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
65                  70                  75                  80


Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
                85                  90                  95


Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
            100                 105                 110


Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Pro Phe Trp
        115                 120                 125


Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
    130                 135                 140


Thr Val Ala Phe Ile Ile Phe Trp Val
145                 150


<210> 150
<211> 163
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 150
Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1               5                   10                  15


Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
            20                  25                  30


Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
        35                  40                  45


Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
    50                  55                  60
```

Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
65 70 75 80

Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
85 90 95

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
100 105 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Ile Thr Leu Ile Ile Phe Gly Val Met Ala
130 135 140

Gly Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg Gly
145 150 155 160

Gly Gly Ser

<210> 151
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 151
Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
35 40 45

Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
    50   55   60

Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
65   70   75   80

Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
                85   90   95

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
            100   105   110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115   120   125

Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly
    130   135   140

Val Ile Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
145   150   155   160

<210> 152
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 152
Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1   5   10   15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
            20   25   30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly

```
        35                  40                  45

Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
    50                  55                  60

Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
65                  70                  75                  80

Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
                85                  90                  95

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
            100                 105                 110

Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly
    130                 135                 140

Val Ile Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
145                 150                 155                 160
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<210> 153
<211> 1284
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
Low-affinity nerve growth factor receptor (LNGFR, TNFRSF16)
sequence

<400> 153
atgggggcag gtgccaccgg ccgcgccatg gacgggccgc gcctgctgct gttgctgctt 60

ctgggggtgt cccttggagg tgccaaggag gcatgcccca caggcctgta cacacacagc 120

ggtgagtgct gcaaagcctg caacctgggc gagggtgtgg cccagccttg tggagccaac 180

cagaccgtgt gtgagccctg cctggacagc gtgacgttct ccgacgtggt gagcgcgacc 240

gagccgtgca agccgtgcac cgagtgcgtg gggctccaga gcatgtcggc gccgtgcgtg 300

gaggccgacg acgccgtgtg ccgctgcgcc tacggctact accaggatga gacgactggg 360

cgctgcgagg cgtgccgcgt gtgcgaggcg ggctcgggcc tcgtgttctc ctgccaggac 420

aagcagaaca ccgtgtgcga ggagtgcccc gacggcacgt attccgacga ggccaaccac 480

gtggacccgt gcctgccctg caccgtgtgc gaggacaccg agcgccagct ccgcgagtgc 540

acacgctggg ccgacgccga gtgcgaggag atccctggcc gttggattac acggtccaca 600

cccccagagg gctcggacag cacagccccc agcacccagg agcctgaggc acctccagaa 660

caagacctca tagccagcac ggtggcaggt gtggtgacca cagtgatggg cagctcccag 720

cccgtggtga cccgaggcac caccgacaac ctcatccctg tctattgctc catcctggct 780

gctgtggttg tgggccttgt ggcctacata gccttcaaga ggtggaacag ctgcaagcag 840

aacaagcaag gagccaacag ccggccagtg aaccagacgc ccccaccaga gggagaaaaa 900

ctccacagcg acagtggcat ctccgtggac agccagagcc tgcatgacca gcagccccac 960

acgcagacag cctcgggcca ggccctcaag ggtgacggag gcctctacag cagcctgccc 1020

ccagccaagc gggaggaggt ggagaagctt ctcaacggct ctgcgggggа cacctggcgg 1080

cacctggcgg gcgagctggg ctaccagccc gagcacatag actcctttac ccatgaggcc 1140

tgccccgttc gcgccctgct tgcaagctgg gccacccagg acagcgccac actggacgcc 1200

ctcctggccg ccctgcgccg catccagcga gccgacctcg tggagagtct gtgcagtgag 1260

tccactgcca catccccggt gtga 1284

<210> 154
<211> 427
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
Low-affinity nerve growth factor receptor (LNGFR, TNFRSF16)
sequence

<400> 154

```
Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu
1               5                   10                  15

Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys
            20                  25                  30

Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn
        35                  40                  45

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys
    50                  55                  60

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
65                  70                  75                  80

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
                85                  90                  95

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
            100                 105                 110

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
        115                 120                 125

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
    130                 135                 140

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
145                 150                 155                 160

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
                165                 170                 175

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
            180                 185                 190

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
```

```
        195                 200                 205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
    210                 215                 220

Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln
225                 230                 235                 240

Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile Pro Val Tyr Cys
                245                 250                 255

Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala Tyr Ile Ala Phe
            260                 265                 270

Lys Arg Trp Asn Ser Cys Lys Gln Asn Lys Gln Gly Ala Asn Ser Arg
        275                 280                 285

Pro Val Asn Gln Thr Pro Pro Pro Glu Gly Glu Lys Leu His Ser Asp
    290                 295                 300

Ser Gly Ile Ser Val Asp Ser Gln Ser Leu His Asp Gln Gln Pro His
305                 310                 315                 320

Thr Gln Thr Ala Ser Gly Gln Ala Leu Lys Gly Asp Gly Gly Leu Tyr
                325                 330                 335

Ser Ser Leu Pro Pro Ala Lys Arg Glu Glu Val Glu Lys Leu Leu Asn
            340                 345                 350

Gly Ser Ala Gly Asp Thr Trp Arg His Leu Ala Gly Glu Leu Gly Tyr
        355                 360                 365

Gln Pro Glu His Ile Asp Ser Phe Thr His Glu Ala Cys Pro Val Arg
    370                 375                 380

Ala Leu Leu Ala Ser Trp Ala Thr Gln Asp Ser Ala Thr Leu Asp Ala
385                 390                 395                 400
```

Leu Leu Ala Ala Leu Arg Arg Ile Gln Arg Ala Asp Leu Val Glu Ser
405 410 415

Leu Cys Ser Glu Ser Thr Ala Thr Ser Pro Val
420 425

<210> 155
<211> 666
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
LNGFR Extracellular Domain (K29-N250) sequence

<400> 155
aaggaggcat gccccacagg cctgtacaca cacagcggtg agtgctgcaa agcctgcaac 60

ctgggcgagg gtgtggccca gccttgtgga gccaaccaga ccgtgtgtga gccctgcctg 120

gacagcgtga cgttctccga cgtggtgagc gcgaccgagc cgtgcaagcc gtgcaccgag 180

tgcgtggggc tccagagcat gtcggcgccg tgcgtggagg ccgacgacgc cgtgtgccgc 240

tgcgcctacg gctactacca ggatgagacg actgggcgct gcgaggcgtg ccgcgtgtgc 300

gaggcgggct cgggcctcgt gttctcctgc caggacaagc agaacaccgt gtgcgaggag 360

tgccccgacg gcacgtattc cgacgaggcc aaccacgtgg acccgtgcct gccctgcacc 420

gtgtgcgagg acaccgagcg ccagctccgc gagtgcacac gctgggccga cgccgagtgc 480

gaggagatcc ctggccgttg gattacacgg tccacacccc cagagggctc ggacagcaca 540

gcccccagca cccaggagcc tgaggcacct ccagaacaag acctcatagc cagcacggtg 600

gcaggtgtgg tgaccacagt gatgggcagc tcccagcccg tggtgacccg aggcaccacc 660

gacaac 666

<210> 156
<211> 222
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
LNGFR Extracellular Domain (K29-N250) sequence

<400> 156

```
Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys
1               5                   10                  15


Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
            20                  25                  30


Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
        35                  40                  45


Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu
    50                  55                  60


Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
65                  70                  75                  80


Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala
                85                  90                  95


Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp
            100                 105                 110


Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
        115                 120                 125


Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp
    130                 135                 140


Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys
145                 150                 155                 160


Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly
                165                 170                 175
```

Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu
180 185 190

Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met
195 200 205

Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
210 215 220

<210> 157
<211> 558
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 157
gagccctgcc tggacagcgt gacgttctcc gacgtggtga gcgcgaccga gccgtgcaag 60

ccgtgcaccg agtgcgtggg gctccagagc atgtcggcgc cgtgcgtgga ggccgacgac 120

gccgtgtgcc gctgcgccta cggctactac caggatgaga cgactgggcg ctgcgaggcg 180

tgccgcgtgt gcgaggcggg ctcgggcctc gtgttctcct gccaggacaa gcagaacacc 240

gtgtgcgagg agtgccccga cggcacgtat tccgacgagg ccaaccacgt ggacccgtgc 300

ctgccctgca ccgtgtgcga ggacaccgag cgccagctcc gcgagtgcac acgctgggcc 360

gacgccgagt gcgaggagat ccctggccgt tggattacac ggtccacacc cccagagggc 420

tcggacagca cagcccccag cacccaggag cctgaggcac ctccagaaca agacctcata 480

gccagcacgg tggcaggtgt ggtgaccaca gtgatgggca gctcccagcc cgtggtgacc 540

cgaggcacca ccgacaac 558

<210> 158
<211> 186
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 158
Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
1 5 10 15

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
20 25 30

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
35 40 45

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
50 55 60

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
65 70 75 80

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
85 90 95

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
100 105 110

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
115 120 125

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
130 135 140

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
145 150 155 160

Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln
165 170 175

Pro Val Val Thr Arg Gly Thr Thr Asp Asn
180 185

<210> 159
<211> 429
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 159
cgctgcgcct acggctacta ccaggatgag acgactgggc gctgcgaggc gtgccgcgtg 60

tgcgaggcgg gctcgggcct cgtgttctcc tgccaggaca agcagaacac cgtgtgcgag 120

gagtgccccg acggcacgta ttccgacgag gccaaccacg tggacccgtg cctgccctgc 180

accgtgtgcg aggacaccga gcgccagctc cgcgagtgca cacgctgggc cgacgccgag 240

tgcgaggaga tccctggccg ttggattaca cggtccacac ccccagaggg ctcggacagc 300

acagccccca gcacccagga gcctgaggca cctccagaac aagacctcat agccagcacg 360

gtggcaggtg tggtgaccac agtgatgggc agctcccagc ccgtggtgac ccgaggcacc 420

accgacaac 429

<210> 160
<211> 143
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 160
Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
1 5 10 15

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
20 25 30

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
35 40 45

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
50 55 60

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
65 70 75 80

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
85 90 95

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
100 105 110

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
115 120 125

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn
130 135 140

<210> 161
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 161
aaggaggcat gccccacagg cctgtacaca cacagcggtg agtgctgcaa agcctgcaac 60

ctgggcgagg gtgtggccca gccttgtgga gccaaccaga ccgtgtgtga gccctgcctg 120

gacagcgtga cgttctccga cgtggtgagc gcgaccgagc cgtgcaagcc gtgcaccgag 180

tgcgtggggc tccagagcat gtcggcgccg tgcgtggagg ccgacgacgc cgtgtgccgc 240

tgcgcctacg gctactacca ggatgagacg actgggcgct gcgaggcgtg ccgcgtgtgc 300

gaggcgggct cgggcctcgt gttctcctgc caggacaagc agaacaccgt gtgcgaggag 360

tgccccgacg gcacgtattc cgacgaggcc aaccacgtgg acccgtgcct gccctgcacc 420

gtgtgcgagg acaccgagcg ccagctccgc gagtgcacac gctgggccga cgccgagtgc 480

gaggagatcc ctggccgttg gattacacgg tccacacccc cagagggctc ggacagcaca 540

gcccccagca cccaggagcc tgaggcacct ccagaacaag acctcatagc cagcacggtg 600

gcaggtgtgg tgaccacagt gatgggcagc tcccagcccg tggtgacccg aggcaccacc 660

gacaacctca tccctgtcta ttgctccatc ctggctgctg tggttgtggg ccttgtggcc 720

tacatagcct tc 732

<210> 162
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 162
Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys
1 5 10 15

Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
20 25 30

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
35 40 45

Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu
50 55 60

Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
65 70 75 80

Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala
85 90 95

```
Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp
            100                 105                 110

Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
        115                 120                 125

Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp
    130                 135                 140

Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys
145                 150                 155                 160

Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly
                165                 170                 175

Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu
            180                 185                 190

Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met
        195                 200                 205

Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Leu Ile
    210                 215                 220

Pro Val Tyr Cys Ser Ile Leu Ala Ala Val Val Val Gly Leu Val Ala
225                 230                 235                 240

Tyr Ile Ala Phe
```

<210> 163
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 163
Lys Glu Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys
1   5   10   15

Lys Ala Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn
            20   25   30

Gln Thr Val Cys Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val
        35   40   45

Val Ser Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu
    50   55   60

Gln Ser Met Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg
65   70   75   80

Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala
                85   90   95

Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp
            100   105   110

Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp
        115   120   125

Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp
    130   135   140

Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys
145   150   155   160

Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly
                165   170   175

Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu
            180   185   190

```
Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met
        195                 200                 205

Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly Gly
    210                 215                 220

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
225                 230                 235                 240

Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr
                245                 250                 255

Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys
            260                 265                 270

Arg Ser
```

<210> 164
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 164

```
Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr
1               5                   10                  15

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser
            20                  25                  30

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly
        35                  40                  45

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys
    50                  55                  60
```

```
Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr
65                  70                  75                  80

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His
                85                  90                  95

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln
            100                 105                 110

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro
        115                 120                 125

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr
    130                 135                 140

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile
145                 150                 155                 160

Ala Ser Thr Val Ala Gly Val Val Thr Thr Val Met Gly Ser Ser Gln
                165                 170                 175

Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly Gly Gly Gly Ser Gly
            180                 185                 190

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp
        195                 200                 205

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
    210                 215                 220

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
225                 230                 235

<210> 165
<211> 195
<212> PRT
```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 165
Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
1 5 10 15

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
20 25 30

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
35 40 45

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
50 55 60

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
65 70 75 80

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
85 90 95

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
100 105 110

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
115 120 125

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
165 170 175

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
180 185 190

Lys Arg Ser
195

<210> 166
<211> 193
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 166
Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
1 5 10 15

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
20 25 30

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
35 40 45

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
50 55 60

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
65 70 75 80

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
85 90 95

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
100 105 110

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val

```
        115                 120                 125

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Glu Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val
                165                 170                 175

Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg Gly Gly Gly
            180                 185                 190

Ser
```

<210> 167
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 167

```
Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
1               5                   10                  15

Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
            20                  25                  30

Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
        35                  40                  45

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
    50                  55                  60
```

```
Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
65                  70                  75                  80


Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
                85                  90                  95


Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
            100                 105                 110


Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
        115                 120                 125


Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly
    130                 135                 140


Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160


Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile
                165                 170                 175


Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
            180                 185                 190


<210> 168
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 168
Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu
1               5                   10                  15


Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln
            20                  25                  30
```

```
Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser
        35                  40                  45

Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu
    50                  55                  60

Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu
65                  70                  75                  80

Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu
                85                  90                  95

Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro
            100                 105                 110

Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val Val Thr Thr Val
        115                 120                 125

Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr Thr Asp Asn Gly
    130                 135                 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile
                165                 170                 175

Gly Thr Ile Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
            180                 185                 190
```

<210> 169
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 169
atggcgctgc ccgtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc 120

accatcagtt gcagggcaag tcaggacatt agtaaatatt taaattggta tcagcagaaa 180

ccagatggaa ctgttaaact cctgatctac catacatcaa gattacactc aggagtccca 240

tcaaggttca gtggcagtgg gtctggaaca gattattctc tcaccattag caatttggag 300

caggaagata ttgccactta cttttgccaa cagggtaata cgcttccgta cacgttcgga 360

gggggggacca agctggagat cacaggtggc ggtggctcgg gcggtggtgg gtcgggtggc 420

ggcggatctg aggtgaaact gcaggagtca ggacctggcc tggtggcgcc ctcacagagc 480

ctgtccgtca catgcactgt ctcaggggtc tcattacccg actatggtgt aagctggatt 540

cgccagcctc cacgaaaggg tctggagtgg ctgggagtaa tatggggtag tgaaaccaca 600

tactataatt cagctctcaa atccagactg accatcatca aggacaactc caagagccaa 660

gttttcttaa aaatgaacag tctgcaaact gatgacacag ccatttacta ctgtgccaaa 720

cattattact acggtggtag ctatgctatg gactactggg gccaaggaac ctcagtcacc 780

gtctcctcaa ccacgacgcc agcgccgcga ccaccaacac cggcgcccac catcgcgtcg 840

cagcccctgt ccctgcgccc agaggcgtgt agaccggctg caggtggagc agtgcacacg 900

agggggctgg acttcgcctg tgatatctac atctgggcgc ccttggccgg gacttgtggg 960

gtccttctcc tgtcactggt tatcaccctt tactgccgcg tcaagttcag caggagcgca 1020

gacgcccccg cgtacaagca gggccagaac cagctctata acgagctcaa tctaggacga 1080

agagaggagt acgatgtttt ggacaagaga cgtggccggg accctgagat gggggggaaag 1140

ccgagaagga agaaccctca ggaaggcctg tacaatgaac tgcagaaaga taagatggcg 1200

gaggcctaca gtgagattgg gatgaaaggc gagcgccgga ggggcaaggg gcacgatggc 1260

ctttaccagg gtctcagtac agccaccaag gacacctacg acgcccttca catgcaggcc 1320

ctgccccctc gc 1332

<210> 170
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 170
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
20 25 30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65 70 75 80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
85 90 95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
100 105 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
130 135 140

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145 150 155 160

```
Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
                165                 170                 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
            180                 185                 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
        195                 200                 205

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
    210                 215                 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225                 230                 235                 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
            260                 265                 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
        275                 280                 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
    290                 295                 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305                 310                 315                 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Val Lys Phe
                325                 330                 335

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu
            340                 345                 350
```

```
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
        355                 360                 365

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
    370                 375                 380

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
385                 390                 395                 400

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
                405                 410                 415

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
            420                 425                 430

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
        435                 440
```

<210> 171
<211> 1467
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 171
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc 120

accatcagtt gcagggcaag tcaggacatt agtaaatatt taaattggta tcagcagaaa 180

ccagatggaa ctgttaaact cctgatctac catacatcaa gattacactc aggagtccca 240

tcaaggttca gtggcagtgg gtctggaaca gattattctc tcaccattag caacctggag 300

caagaagata ttgccactta cttttgccaa cagggtaata cgcttccgta cacgttcgga 360

gggggggacca agctggagat cacaggcagc acctccggca gcggcaagcc tggcagcggc 420

gagggcagca ccaagggcga ggtgaaactg caggagtcag gacctggcct ggtggcgccc 480

tcacagagcc tgtccgtcac atgcactgtc tcaggggtct cattacccga ctatggtgta 540

agctggattc gccagcctcc acgaaagggt ctggagtggc tgggagtaat atggggtagt 600

gaaaccacat actataattc agctctcaaa tccagactga ccatcatcaa ggacaactcc 660

aagagccaag ttttcttaaa aatgaacagt ctgcaaactg atgacacagc catttactac 720

tgtgccaaac attattacta cggtggtagc tatgctatgg actactgggg ccaaggaacc 780

tcagtcaccg tctcctcaac cacgacgcca gcgccgcgac caccaacacc ggcgcccacc 840

atcgcgtcgc agcccctgtc cctgcgccca gaggcgtgcc ggccagcggc gggggcgcga 900

gtgcacacga gggggctgga cttcgcctgt gatatctaca tctgggcgcc cttggccggg 960

acttgtgggg tccttctcct gtcactggtt atcacccttt actgcaaacg gggcagaaag 1020

aaactcctgt atatattcaa acaaccattt atgagaccag tacaaactac tcaagaggaa 1080

gatggctgta gctgccgatt tccagaagaa gaagaaggag gatgtgaact gagagtgaag 1140

ttcagcagga gcgcagacgc ccccgcgtac aagcagggcc agaaccagct ctataacgag 1200

ctcaatctag gacgaagaga ggagtacgat gttttggaca agagacgtgg ccgggaccct 1260

gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgtacaa tgaactgcag 1320

aaagataaga tggcggaggc ctacagtgag attgggatga aaggcgagcg ccggaggggc 1380

aaggggcacg atggccttta ccagggtctc agtacagcca ccaaggacac ctacgacgcc 1440

cttcacatgc aggccctgcc ccctcgc 1467

<210> 172
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 172
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

```
His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
    130                 135                 140

Lys Gly Glu Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro
145                 150                 155                 160

Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro
                165                 170                 175

Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu
            180                 185                 190

Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala
        195                 200                 205
```

```
Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val
    210                 215                 220

Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr
225                 230                 235                 240

Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp
                245                 250                 255

Gly Gln Gly Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro
            260                 265                 270

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
        275                 280                 285

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
    290                 295                 300

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
305                 310                 315                 320

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys
                325                 330                 335

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
            340                 345                 350

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
        355                 360                 365

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
    370                 375                 380

Ala Asp Ala Pro Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu
385                 390                 395                 400

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
```

405 410 415

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
420 425 430

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
435 440 445

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
450 455 460

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
465 470 475 480

Leu His Met Gln Ala Leu Pro Pro Arg
485

<210> 173
<211> 1455
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 173
atggcgctgc ccgtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccggacatcc agatgacaca gactacatcc tccctgtctg cctctctggg agacagagtc 120

accatcagtt gcagggcaag tcaggacatt agtaaatatt taaattggta tcagcagaaa 180

ccagatggaa ctgttaaact cctgatctac catacatcaa gattacactc aggagtccca 240

tcaaggttca gtggcagtgg gtctggaaca gattattctc tcaccattag caatttggag 300

caggaagata ttgccactta cttttgccaa cagggtaata cgcttccgta cacgttcgga 360

gggggggacca agctggagat cacaggtggc ggtggctcgg gcggtggtgg gtcgggtggc 420

ggcggatctg aggtgaaact gcaggagtca ggacctggcc tggtggcgcc ctcacagagc 480

ctgtccgtca catgcactgt ctcaggggtc tcattacccg actatggtgt aagctggatt 540

cgccagcctc cacgaaaggg tctggagtgg ctgggagtaa tatggggtag tgaaaccaca 600

tactataatt cagctctcaa atccagactg accatcatca aggacaactc caagagccaa 660

gttttcttaa aaatgaacag tctgcaaact gatgacacag ccatttacta ctgtgccaaa 720

cattattact acggtggtag ctatgctatg gactactggg gccaaggaac ctcagtcacc 780

gtctcctcaa ccacgacgcc agcgccgcga ccaccaacac cggcgcccac catcgcgtcg 840

cagcccctgt ccctgcgccc agaggcgtgt agaccggctg caggtggagc agtgcacacg 900

agggggctgg acttcgcctg tgatatctac atctgggcgc ccttggccgg gacttgtggg 960

gtccttctcc tgtcactggt tatcaccctt tactgcagga gtaagaggag caggctcctg 1020

cacagtgact acatgaacat gactccccgc cgccccgggc ccacccgcaa gcattaccag 1080

ccctatgccc caccacgcga cttcgcagcc tatcgctccc gcgtcaagtt cagcaggagc 1140

gcagacgccc ccgcgtacaa gcagggccag aaccagctct ataacgagct caatctagga 1200

cgaagagagg agtacgatgt tttggacaag agacgtggcc gggaccctga gatgggggga 1260

aagccgagaa ggaagaaccc tcaggaaggc ctgtacaatg aactgcagaa agataagatg 1320

gcggaggcct acagtgagat tgggatgaaa ggcgagcgcc ggaggggcaa ggggcacgat 1380

ggcctttacc agggtctcag tacagccacc aaggacacct acgacgccct tcacatgcag 1440

gccctgcccc ctcgc 1455

<210> 174
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 174
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

```
His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu
            20                  25                  30

Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln
        35                  40                  45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr
    50                  55                  60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile
                85                  90                  95

Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
    130                 135                 140

Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser
145                 150                 155                 160

Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
                165                 170                 175

Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly
            180                 185                 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
        195                 200                 205

Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys
```

```
    210                 215                 220

Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys
225                 230                 235                 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
            260                 265                 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
        275                 280                 285

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
    290                 295                 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305                 310                 315                 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Ser Lys Arg
                325                 330                 335

Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
            340                 345                 350

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
        355                 360                 365

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
    370                 375                 380

Ala Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
385                 390                 395                 400

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
                405                 410                 415
```

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
420 425 430

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
435 440 445

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
450 455 460

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
465 470 475 480

Ala Leu Pro Pro Arg
485

<210> 175
<211> 2031
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 175
atgctgctgc tggtgaccag cctgctgctg tgtgagctgc cccaccccgc ctttctgctg 60

atccccgaca tccagatgac ccagaccacc tccagcctga gcgccagcct gggcgaccgg 120

gtgaccatca gctgccgggc cagccaggac atcagcaagt acctgaactg gtatcagcag 180

aagcccgacg gcaccgtcaa gctgctgatc taccacacca gccggctgca cagcggcgtg 240

cccagccggt ttagcggcag cggctccggc accgactaca gcctgaccat ctccaacctg 300

gagcaggagg acatcgccac ctacttttgc cagcagggca acacactgcc ctacaccttt 360

ggcggcggaa caaagctgga gatcaccggc agcacctccg gcagcggcaa gcctggcagc 420

ggcgagggca gcaccaaggg cgaggtgaag ctgcaggaga gcggccctgg cctggtggcc 480

cccagccaga gcctgagcgt gacctgtacc gtgtccggcg tgtccctgcc cgactacggc 540

gtgtcctgga tccggcagcc ccctaggaag ggcctggagt ggctgggcgt gatctggggc 600

agcgagacca cctactacaa cagcgccctg aagagccggc tgaccatcat caaggacaac 660

agcaagagcc aggtgttcct gaagatgaac agcctgcaga ccgacgacac cgccatctac 720

tactgtgcca agcactacta ctacggcggc agctacgcca tggactactg gggccagggc 780

accagcgtga ccgtgtccag cgagagcaag tacggccctc cctgcccccc ttgccctgcc 840

cccgagttcc tgggcggacc cagcgtgttc ctgttccccc ccaagcccaa ggacaccctg 900

atgatcagcc ggacccccga ggtgacctgt gtggtggtgg acgtgtccca ggaggacccc 960

gaggtccagt tcaactggta cgtggacggc gtggaggtgc acaacgccaa gaccaagccc 1020

cgggaggagc agttcaatag cacctaccgg gtggtgtccg tgctgaccgt gctgcaccag 1080

gactggctga acggcaagga atacaagtgt aaggtgtcca acaagggcct gcccagcagc 1140

atcgagaaaa ccatcagcaa ggccaagggc cagcctcggg agccccaggt gtacaccctg 1200

ccccctagcc aagaggagat gaccaagaat caggtgtccc tgacctgcct ggtgaagggc 1260

ttctacccca gcgacatcgc cgtggagtgg gagagcaacg gccagcccga gaacaactac 1320

aagaccaccc cccctgtgct ggacagcgac ggcagcttct tcctgtacag caggctgacc 1380

gtggacaaga gccggtggca ggagggcaac gtctttagct gctccgtgat gcacgaggcc 1440

ctgcacaacc actacaccca gaagagcctg tccctgagcc tgggcaagat gttctgggtg 1500

ctggtcgtgg tgggtggcgt gctggcctgc tacagcctgc tggtgacagt ggccttcatc 1560

atcttttggg tgaggagcaa gcggagcaga ggcggccaca gcgactacat gaacatgacc 1620

ccccggaggc ctggccccac ccggaagcac taccagccct acgcccctcc cagggacttc 1680

gccgcctacc ggagccgggt gaagttcagc cggagcgccg acgcccctgc ctaccagcag 1740

ggccagaacc agctgtacaa cgagctgaac ctgggccgga gggaggagta cgacgtgctg 1800

gacaagcgga gaggccggga ccctgagatg ggcggcaagc cccggagaaa gaaccctcag 1860

gagggcctgt ataacgaact gcagaaagac aagatggccg aggcctacag cgagatcggc 1920

atgaagggcg agcggcggag gggcaagggc cacgacggcc tgtaccaggg cctgagcacc 1980

gccaccaagg atacctacga cgccctgcac atgcaggccc tgcccccag a 2031

<210> 176
<211> 677
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 176
Met Leu Leu Leu Val Thr Ser Leu Leu Leu Cys Glu Leu Pro His Pro
1 5 10 15

Ala Phe Leu Leu Ile Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser
20 25 30

Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser
35 40 45

Gln Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly
50 55 60

Thr Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val
65 70 75 80

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr
85 90 95

Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln
100 105 110

Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
115 120 125

Thr Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser
130 135 140

```
Thr Lys Gly Glu Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala
145                 150                 155                 160


Pro Ser Gln Ser Leu Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu
                165                 170                 175


Pro Asp Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu
            180                 185                 190


Glu Trp Leu Gly Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser
        195                 200                 205


Ala Leu Lys Ser Arg Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln
    210                 215                 220


Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr
225                 230                 235                 240


Tyr Cys Ala Lys His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr
                245                 250                 255


Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Glu Ser Lys Tyr Gly
            260                 265                 270


Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser
        275                 280                 285


Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
    290                 295                 300


Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
305                 310                 315                 320


Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
                325                 330                 335


Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
```

```
            340                 345                 350

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
        355                 360                 365

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
    370                 375                 380

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
385                 390                 395                 400

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
                405                 410                 415

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
            420                 425                 430

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
        435                 440                 445

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
    450                 455                 460

Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
465                 470                 475                 480

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
                485                 490                 495

Met Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser
            500                 505                 510

Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg
        515                 520                 525

Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro
    530                 535                 540
```

Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe
545 550 555 560

Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
565 570 575

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
580 585 590

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
595 600 605

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
610 615 620

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
625 630 635 640

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
645 650 655

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
660 665 670

Ala Leu Pro Pro Arg
675

<210> 177
<211> 1131
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 177
aactgggtga atgtgatcag cgacctgaag aagatcgagg atctgatcca gagcatgcac 60

attgatgcca ccctgtacac agaatctgat gtgcacccta gctgtaaagt gaccgccatg 120

aagtgttttc tgctggagct gcaggtgatt tctctggaaa gcggagatgc ctctatccac 180

gacacagtgg agaatctgat catcctggcc aacaatagcc tgagcagcaa tggcaatgtg 240

acagagtctg gctgtaagga gtgtgaggag ctggaggaga agaacatcaa ggagtttctg 300

cagagctttg tgcacatcgt gcagatgttc atcaatacaa gctctggcgg aggatctgga 360

ggaggcggat ctggaggagg aggcagtgga ggcggaggat ctggcggagg atctctgcag 420

attacatgcc ctcctccaat gtctgtggag cacgccgata tttgggtgaa gtcctacagc 480

ctgtacagca gagagagata catctgcaac agcggcttta agagaaaggc cggcacctct 540

tctctgacag agtgcgtgct gaataaggcc acaaatgtgg cccactggac aacacctagc 600

ctgaagtgca ttagagatcc tgccctggtc caccagaggc ctgcccctcc atctacagtg 660

acaacagccg gagtgacacc tcagcctgaa tctctgagcc cttctggaaa agaacctgcc 720

gccagctctc ctagctctaa taataccgcc gccacaacag ccgccattgt gcctggatct 780

cagctgatgc ctagcaagtc tcctagcaca ggcacaacag agatcagcag ccacgaatct 840

tctcacggaa caccttctca gaccaccgcc aagaattggg agctgacagc ctctgcctct 900

caccagcctc caggagtgta tcctcagggc cactctgata caacagtggc catcagcaca 960

tctacagtgc tgctgtgtgg actgtctgcc gtgtctctgc tggcctgtta cctgaagtct 1020

agacagacac ctcctctggc ctctgtggag atggaggcca tggaagccct gcctgtgaca 1080

tggggaacaa gcagcagaga tgaggacctg gagaattgtt ctcaccacct g 1131

<210> 178
<211> 377
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 178
Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile

```
1               5                   10                  15

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
            20                  25                  30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
        35                  40                  45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
    50                  55                  60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
65                  70                  75                  80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
                85                  90                  95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
            100                 105                 110

Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ile Thr Cys Pro
    130                 135                 140

Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser
145                 150                 155                 160

Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys
                165                 170                 175

Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn
            180                 185                 190

Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro Ala
        195                 200                 205
```

```
Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val Thr Thr Ala Gly
    210                 215                 220

Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly Lys Glu Pro Ala
225                 230                 235                 240

Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr Thr Ala Ala Ile
                245                 250                 255

Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro Ser Thr Gly Thr
            260                 265                 270

Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr Pro Ser Gln Thr
        275                 280                 285

Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser His Gln Pro Pro
    290                 295                 300

Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr Val Ala Ile Ser Thr
305                 310                 315                 320

Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser Leu Leu Ala Cys
                325                 330                 335

Tyr Leu Lys Ser Arg Gln Thr Pro Pro Leu Ala Ser Val Glu Met Glu
            340                 345                 350

Ala Met Glu Ala Leu Pro Val Thr Trp Gly Thr Ser Ser Arg Asp Glu
        355                 360                 365

Asp Leu Glu Asn Cys Ser His His Leu
    370                 375
```

<210> 179
<211> 841
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 179
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

```
Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
    290                 295                 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
305                 310                 315                 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
                325                 330                 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
            340                 345                 350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
        355                 360                 365
```

```
Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
    370                 375                 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
385                 390                 395                 400

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
                405                 410                 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
            420                 425                 430

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
        435                 440                 445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
    450                 455                 460

Leu Pro Pro Arg Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
465                 470                 475                 480

Glu Glu Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu
                485                 490                 495

Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly
            500                 505                 510

Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn
        515                 520                 525

Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile
    530                 535                 540

Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu
545                 550                 555                 560
```

```
Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly
                565                 570                 575

Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala
            580                 585                 590

Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln
        595                 600                 605

Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg
    610                 615                 620

Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys
625                 630                 635                 640

Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr
                645                 650                 655

Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys
            660                 665                 670

Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys
        675                 680                 685

Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg
    690                 695                 700

Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg
705                 710                 715                 720

Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu
                725                 730                 735

Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys
            740                 745                 750

Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys
```

```
        755                 760                 765

Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala
    770                 775                 780

Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly
785                 790                 795                 800

Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile
                805                 810                 815

Pro Ser Ile Ala Thr Gly Met Val Gly Ala Leu Leu Leu Leu Leu Val
            820                 825                 830

Val Ala Leu Gly Ile Gly Leu Phe Met
        835                 840


<210> 180
<211> 750
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 180
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

```
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
```

```
            260                 265                 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
    290                 295                 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
305                 310                 315                 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
                325                 330                 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
            340                 345                 350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
        355                 360                 365

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
    370                 375                 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
385                 390                 395                 400

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
                405                 410                 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
            420                 425                 430

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
        435                 440                 445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
    450                 455                 460
```

```
Leu Pro Pro Arg Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
465                 470                 475                 480

Glu Glu Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu
                485                 490                 495

Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly
            500                 505                 510

Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn
        515                 520                 525

Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile
    530                 535                 540

Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu
545                 550                 555                 560

Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly
                565                 570                 575

Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala
            580                 585                 590

Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln
        595                 600                 605

Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg
    610                 615                 620

Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys
625                 630                 635                 640

Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr
                645                 650                 655
```

Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys
            660   665   670

Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys
        675   680   685

Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly Ser Gly
    690   695   700

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp
705   710   715   720

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
                725   730   735

Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
            740   745   750

<210> 181
<211> 2814
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polynucleotide

<400> 181
gacatccaaa tgacacagac aaccagcagc ctctctgcca gtctgggaga tcgtgtgacc 60

atcagttgta gagcctcaca agatatttcc aaatacctaa actggtatca gcaaaaacca 120

gatggtacag tgaagttact gatctaccat actagccgtc ttcattccgg tgtgccttct 180

cgctttagcg ggtctggatc aggaacagat tacagtctca ccatcagcaa cctcgaacaa 240

gaagatatag ctacctattt ctgccagcag ggtaacactt tgccatatac cttcggagga 300

ggcacaaaac tggagatcac tggttctacc agtggaagcg gcaagcctgg ctccggtgaa 360

ggaagtacca aaggcgaagt gaagctgcaa gagtcaggtc caggtttggt agctcccagc 420

caatccctat ctgttacctg tacagtgtct ggtgtgtcac ttccagatta tggcgtgtca 480

tggataaggc agcccccacg aaaaggcctg gaatggttgg gggtgatctg gggatctgag 540

accacctact acaacagcgc cctgaaaagt cggctcacca tcatcaaaga caactccaag 600

tcacaagtgt ttcttaagat gaactcactt cagaccgacg acacagccat atactactgt 660

gctaaacatt actactatgg cggtagctat gccatggatt actggggtca aggtactagt 720

gtgacagtat catctgaatc aaagtatggc ccaccctgcc ccccttgtcc cgctcctgag 780

ttcctgggtg gtccctccgt attcctgttt ccacctaagc caaaagacac tctcatgatc 840

agcagaacac ctgaggtgac atgcgtcgta gttgatgtta gccaggagga ccccgaagtg 900

caatttaact ggtacgtaga cggtgtggaa gtgcataacg caaagaccaa gccacgtgaa 960

gagcagttta actccaccta ccgagtggtg tctgtgctca cagtcttaca tcaagattgg 1020

ctgaacggaa aagagtataa atgtaaagta tccaataagg gccttccctc tagcatcgaa 1080

aagactatct ccaaagccaa gggacagcca cgcgaaccac aggtgtatac tttacctcct 1140

tctcaagaag agatgaccaa gaaccaagta tctctgacgt gtttggtgaa ggggttctac 1200

ccctctgaca tcgcagtgga atgggaatca aacggtcaac ctgagaacaa ttacaaaacc 1260

accccacctg tgctggatag cgacggcagc ttctttctgt atagcaggct cacagtggat 1320

aaaagtcggt ggcaggaagg aaacgtattt agttgcagtg tgatgcacga ggccctccat 1380

aaccattata cccagaagtc actctcactt agtctgggta agatgttctg ggtgctcgtg 1440

gtcgtaggtg gagtgctggc ttgctactcc ctcttagtga ccgtggcttt tatcatcttc 1500

tgggtacgtt ccaaaaggtc ccgtggtggc cattcagatt acatgaatat gacccccaga 1560

cgaccaggcc caacaaggaa gcattatcaa ccttacgccc ctccccgaga ttttgcagct 1620

tatcgaagta gggtgaagtt cagccggtct gctgacgctc ctgcatacca gcaaggtcag 1680

aatcagttat acaatgagct aaatctagga cgacgcgaag aatatgatgt gctggacaaa 1740

cgacgtggca gggaccctga aatgggtggc aagccaagaa ggaagaaccc acaagagggt 1800

ctgtacaacg agttgcagaa agacaagatg gcagaggcct actccgagat cggaatgaaa 1860

ggagagaggc ggaggggtaa aggacatgac ggtctttacc agggcctgag cacagctact 1920

aaagatacct acgacgccct ccacatgcag gctttgcccc cacgagctac caattttagt 1980

ctgttgaaac aagctggaga tgtcgaggaa aatccaggcc caatgcgact tcctgctcaa 2040

ctgctgggtc tgctcatgct gtgggttcct ggaagcagtg gccgaaaggt ctgcaacggc 2100

atcggtatcg gcgaatttaa ggatagtcta tctatcaacg ctaccaatat taagcatttt 2160

aagaactgca cgtctatttc cggcgacttg cacatcctcc ctgttgcatt tcggggtgat 2220

agtttcaccc ataccccccc tctcgatcca caagaactgg acattcttaa aaccgttaaa 2280

gaaataacag gttttctcct catccaggca tggcccgaga ataggacaga tcttcacgca 2340

tttgaaaacc tcgaaatcat cagagggagg accaaacagc atggtcagtt tagtctcgca 2400

gtggtgtctc tgaacatcac ttctttaggg cttcgatcac ttaaggaaat ctctgacggt 2460

gatgtaatca tcagcggtaa caagaacctg tgctacgcta acacgatcaa ctggaagaag 2520

ctgtttggca caagcggcca gaaaaccaag atcattagta ataggggcga gaatagctgt 2580

aaagcaaccg ggcaagtgtg tcacgctctg tgttctcccg agggatgttg gggacctgaa 2640

ccaagagact gcgttagtgg agggggggc tctggtggcg gaggatctgg cggaggcgga 2700

agcggaggcg gggggagctt ctgggtgctc gtggtcgtag gaggggtgct ggcctgttac 2760

tctctactcg taactgttgc tttcatcata ttctgggtcc gaagtaagcg tagc 2814

<210> 182
<211> 938
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 182
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

```
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220
```

```
Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
    370                 375                 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
```

```
            420                 425                 430

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val
465                 470                 475                 480

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
                485                 490                 495

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser
            500                 505                 510

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
        515                 520                 525

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
    530                 535                 540

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
545                 550                 555                 560

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
                565                 570                 575

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
            580                 585                 590

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
        595                 600                 605

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
    610                 615                 620
```

```
Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
625                 630                 635                 640

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala
                645                 650                 655

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
            660                 665                 670

Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp
        675                 680                 685

Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
    690                 695                 700

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
705                 710                 715                 720

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
                725                 730                 735

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
            740                 745                 750

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
        755                 760                 765

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
    770                 775                 780

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
785                 790                 795                 800

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
                805                 810                 815
```

```
Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
            820                 825                 830

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
        835                 840                 845

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
    850                 855                 860

Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu
865                 870                 875                 880

Pro Arg Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                885                 890                 895

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val
            900                 905                 910

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
        915                 920                 925

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
    930                 935


<210> 183
<211> 959
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 183
Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1               5                   10                  15

Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe
            20                  25                  30
```

```
Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn
        35                  40                  45

Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg
    50                  55                  60

Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp
65                  70                  75                  80

Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala
                85                  90                  95

Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile
            100                 105                 110

Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val
        115                 120                 125

Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser
    130                 135                 140

Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn
145                 150                 155                 160

Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys
                165                 170                 175

Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val
            180                 185                 190

Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg
        195                 200                 205

Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    210                 215                 220
```

```
Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly
225                 230                 235                 240

Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
                245                 250                 255

Phe Trp Val Arg Ser Lys Arg Ser Ala Thr Asn Phe Ser Leu Leu Lys
            260                 265                 270

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val
        275                 280                 285

Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro
    290                 295                 300

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
305                 310                 315                 320

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
                325                 330                 335

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
            340                 345                 350

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
        355                 360                 365

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
    370                 375                 380

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
385                 390                 395                 400

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
                405                 410                 415
```

```
Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
            420                 425                 430

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
        435                 440                 445

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
    450                 455                 460

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
465                 470                 475                 480

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
                485                 490                 495

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
            500                 505                 510

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
        515                 520                 525

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
    530                 535                 540

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
545                 550                 555                 560

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
                565                 570                 575

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
            580                 585                 590

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
        595                 600                 605

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
```

```
    610                 615                 620

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
625                 630                 635                 640

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
                645                 650                 655

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
            660                 665                 670

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
        675                 680                 685

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
    690                 695                 700

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
705                 710                 715                 720

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
                725                 730                 735

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
            740                 745                 750

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
        755                 760                 765

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val
    770                 775                 780

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
785                 790                 795                 800

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser
                805                 810                 815
```

```
Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
            820                 825                 830

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
        835                 840                 845

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
    850                 855                 860

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
865                 870                 875                 880

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
                885                 890                 895

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
            900                 905                 910

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
        915                 920                 925

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
    930                 935                 940

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
945                 950                 955
```

<210> 184
<211> 763
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 184

```
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
```

```
1               5                   10                  15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205
```

```
Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
                245                 250                 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
    290                 295                 300

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
305                 310                 315                 320

Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
                325                 330                 335

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            340                 345                 350

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
        355                 360                 365

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
    370                 375                 380

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
385                 390                 395                 400
```

```
Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
                405                 410                 415

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
            420                 425                 430

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
        435                 440                 445

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
    450                 455                 460

Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Lys Arg Ser Gly Ser
465                 470                 475                 480

Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn
                485                 490                 495

Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu
            500                 505                 510

Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile
        515                 520                 525

Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His
    530                 535                 540

Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val
545                 550                 555                 560

Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln
                565                 570                 575

Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu
            580                 585                 590
```

```
Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn
        595                 600                 605

Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu
    610                 615                 620

Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys
625                 630                 635                 640

Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys
                645                 650                 655

Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln
            660                 665                 670

Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr
        675                 680                 685

Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro
    690                 695                 700

Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
705                 710                 715                 720

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val
                725                 730                 735

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
            740                 745                 750

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
        755                 760
```

<210> 185
<211> 2553
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 185
gacatacaga tgactcagac aacaagtagc ttgtccgcat ccctgggcga tagagtgacc 60

atcagttgtc gagcatccca agatatatcc aagtacttaa actggtatca gcagaagcca 120

gatggcaccg tcaagctgct aatctaccac acaagtaggc tccacagcgg agtgcctagc 180

cgattctctg gttctggttc tggcacagac tattccctaa ccatcagcaa cctggagcaa 240

gaggacattg caacatattt ttgccagcag ggcaacacac tgccatatac ctttggaggc 300

gggaccaagc tggaaatcac cggtagtacg agtggttctg gaaaacctgg ttctggcgaa 360

ggtagtacta aaggagaggt gaaacttcaa gagagtggcc ctggcttggt ggcccttct 420

caaagtttga gcgtgacctg cacagtaagt ggcgtcagcc tgccagatta cggagtcagt 480

tggattcgcc agcctccaag gaagggcctt gaatggctgg gcgtaatctg ggggtccgaa 540

accacctatt acaactccgc acttaagagc cgtttaacca tcatcaaaga caacagcaag 600

agtcaggtct ttctcaaaat gaatagtctg caaacggacg acaccgctat ctactattgt 660

gccaagcact actactatgg tggctcctac gctatggatt actggggaca aggaacaagc 720

gtgacagtgt caagtactac cacacctgct ccccgtcctc caacccccgc tcctactatt 780

gccagtcaac cactgtctct taggcccgag gcatgtaggc cagcagcagg cggggctgtg 840

catacccgag gtctcgactt cgcctgcgac atatatatct gggcccctct ggctggcact 900

tgtggggtcc tcctcctgag tctcgtgatc actctgtatt gtaaacgtgg gcgaaagaag 960

ctcctttaca tcttcaagca acccttcatg aggcctgtac agaccacgca ggaggaggac 1020

gggtgtagtt gccgattccc cgaagaggaa gaaggcggtt gcgagcttcg agtgaaattc 1080

agtaggagtg ctgacgcacc agcatataag cagggccaga accaattata caacgagctg 1140

aacctcggac gaagggaaga gtatgatgtg ctggataagc gcagaggccg tgatccagaa 1200

atgggcggca aacctcgtcg gaaaaatcca caagaggggc tatacaacga attgcagaaa 1260

gacaaaatgg cagaggccta ttctgaaatc ggcatgaagg gcgaacgacg aagaggtaag 1320

ggtcatgacg gcctgtatca aggtctctct accgccacaa aggacactta cgatgcttta 1380

cacatgcagg ctctccctcc cagacaatgc accaactacg ctctattgaa gttggcagga 1440

gatgtggaat ccaaccccgg tcctatgcgt ctacctgccc agctgcttgg gctcctgatg 1500

ctgtgggtcc ccggcagcag tggtagaaaa gtatgtaacg gcataggtat cggtgaattt 1560

aaggactcac taagcatcaa cgccacaaac atcaagcact ttaagaactg tacctctatt 1620

agcggagact tacacatcct gccagtcgca tttcgaggag acagtttcac ccacactcca 1680

cctctcgatc ctcaggaatt agacattctt aaaacagtta aggaaatcac tggatttctt 1740

cttatccagg cctggccaga aaatagaaca gacctgcacg ctttcgagaa ccttgaaata 1800

atacgaggca ggaccaaaca gcatggccaa tttagtttgg ctgtagtctc cttgaacatc 1860

acttcccttg gcctaaggtc tttgaaggaa atcagtgacg gagacgtgat tatcagcggg 1920

aacaagaacc tctgttacgc aaacacaatc aactggaaga agctctttgg caccagcggc 1980

cagaagacaa agatcatttc taaccgagga gagaacagtt gtaaggcaac aggacaagtg 2040

tgccacgctt tgtgcagccc cgagggatgt tggggtcctg agccacgtga ttgtgtctct 2100

tgccggaacg tcagcagagg tagagaatgt gtggataagt gcaacctcct ggaaggggag 2160

cctcgtgagt tcgtggagaa ctccgaatgt atccagtgtc atccagaatg cctgccccag 2220

gccatgaaca taacatgtac aggacgcggc ccagacaact gcatacagtg cgcccactac 2280

attgatggcc cccattgcgt aaagacttgt cctgctggag tcatgggcga aaataacacc 2340

ctggtgtgga agtacgccga cgctggccat gtatgtcatc tgtgtcatcc taattgcacc 2400

tatggctgca ctggccccgg ccttgaagga tgccccggcg gtggaggagg aggctctttc 2460

tgggtcctcg tggtggtggg aggcgtgctg gcctgctatt ccttgctggt cacggtcgcc 2520

ttcattattt tctgggtgag atctaaaaga agc 2553

<210> 186
<211> 851
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 186
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu

```
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
    290                 295                 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
305                 310                 315                 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
                325                 330                 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
            340                 345                 350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
        355                 360                 365

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
    370                 375                 380
```

```
Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
385                 390                 395                 400

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
                405                 410                 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
            420                 425                 430

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
        435                 440                 445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
    450                 455                 460

Leu Pro Pro Arg Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly
465                 470                 475                 480

Asp Val Glu Ser Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu
                485                 490                 495

Gly Leu Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys
            500                 505                 510

Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala
        515                 520                 525

Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu
    530                 535                 540

His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro
545                 550                 555                 560

Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile
                565                 570                 575
```

```
Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu
            580                 585                 590

His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His
        595                 600                 605

Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly
    610                 615                 620

Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly
625                 630                 635                 640

Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe
                645                 650                 655

Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn
            660                 665                 670

Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu
        675                 680                 685

Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Cys Arg Asn Val
    690                 695                 700

Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu Leu Glu Gly Glu
705                 710                 715                 720

Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln Cys His Pro Glu
                725                 730                 735

Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly Arg Gly Pro Asp
            740                 745                 750

Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro His Cys Val Lys
        755                 760                 765
```

```
Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr Leu Val Trp Lys
    770                 775                 780

Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His Pro Asn Cys Thr
785                 790                 795                 800

Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro Gly Gly Gly Gly
                805                 810                 815

Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys
            820                 825                 830

Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
        835                 840                 845

Lys Arg Ser
    850
```

<210> 187
<211> 761
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 187

```
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

```
Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
                245                 250                 255
```

```
Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
    290                 295                 300

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
305                 310                 315                 320

Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
                325                 330                 335

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            340                 345                 350

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
        355                 360                 365

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
    370                 375                 380

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
385                 390                 395                 400

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
                405                 410                 415

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
            420                 425                 430

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
        435                 440                 445

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
```

```
    450                 455                 460

Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Lys Arg Ser Gly Ser
465                 470                 475                 480

Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn
                485                 490                 495

Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu
            500                 505                 510

Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile
        515                 520                 525

Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His
    530                 535                 540

Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val
545                 550                 555                 560

Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln
                565                 570                 575

Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu
            580                 585                 590

Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn
        595                 600                 605

Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu
    610                 615                 620

Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys
625                 630                 635                 640

Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys
                645                 650                 655
```

```
Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln
            660                 665                 670


Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr
        675                 680                 685


Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro
    690                 695                 700


Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
705                 710                 715                 720


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Thr Leu Ile
                725                 730                 735


Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ile Ser
            740                 745                 750


Tyr Gly Ile Arg Arg Gly Gly Gly Ser
        755                 760


<210> 188
<211> 750
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 188
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
```

```
        35                  40                  45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240
```

```
Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
    290                 295                 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
305                 310                 315                 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
                325                 330                 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
            340                 345                 350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
        355                 360                 365

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
    370                 375                 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
385                 390                 395                 400

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
                405                 410                 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
            420                 425                 430
```

```
Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
        435                 440                 445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
    450                 455                 460

Leu Pro Pro Arg Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly
465                 470                 475                 480

Asp Val Glu Ser Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu
                485                 490                 495

Gly Leu Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys
            500                 505                 510

Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala
        515                 520                 525

Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu
    530                 535                 540

His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro
545                 550                 555                 560

Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile
                565                 570                 575

Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu
            580                 585                 590

His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His
        595                 600                 605

Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly
    610                 615                 620
```

```
Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly
625                 630                 635                 640


Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe
                645                 650                 655


Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn
            660                 665                 670


Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu
        675                 680                 685


Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly
    690                 695                 700


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
705                 710                 715                 720


Glu Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr
                725                 730                 735


Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg Gly Gly Gly Ser
            740                 745                 750


<210> 189
<211> 758
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 189
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15


Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30
```

```
Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220
```

```
Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
                245                 250                 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
    290                 295                 300

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
305                 310                 315                 320

Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
                325                 330                 335

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            340                 345                 350

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
        355                 360                 365

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
    370                 375                 380

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
385                 390                 395                 400

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
                405                 410                 415

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
```

```
            420                 425                 430

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
        435                 440                 445

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
    450                 455                 460

Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Lys Arg Ser Gly Ser
465                 470                 475                 480

Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn
                485                 490                 495

Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu
            500                 505                 510

Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile
        515                 520                 525

Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His
    530                 535                 540

Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val
545                 550                 555                 560

Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln
                565                 570                 575

Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu
            580                 585                 590

Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn
        595                 600                 605

Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu
    610                 615                 620
```

Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys
625 630 635 640

Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys
645 650 655

Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln
660 665 670

Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr
675 680 685

Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro
690 695 700

Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
705 710 715 720

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile
725 730 735

Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr
740 745 750

Gly Ile Gly Gly Gly Ser
755

<210> 190
<211> 747
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 190
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly

```
1               5                   10                  15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205
```

```
Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
    290                 295                 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
305                 310                 315                 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
                325                 330                 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
            340                 345                 350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
        355                 360                 365

Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
    370                 375                 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
385                 390                 395                 400
```

```
Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
                405                 410                 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
            420                 425                 430

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
        435                 440                 445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
    450                 455                 460

Leu Pro Pro Arg Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly
465                 470                 475                 480

Asp Val Glu Ser Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu
                485                 490                 495

Gly Leu Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys
            500                 505                 510

Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala
        515                 520                 525

Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu
    530                 535                 540

His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro
545                 550                 555                 560

Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile
                565                 570                 575

Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu
            580                 585                 590
```

```
His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His
        595                 600                 605

Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly
    610                 615                 620

Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly
625                 630                 635                 640

Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe
                645                 650                 655

Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn
            660                 665                 670

Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu
        675                 680                 685

Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly
    690                 695                 700

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
705                 710                 715                 720

Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile
                725                 730                 735

Leu Leu Ile Ser Tyr Gly Ile Gly Gly Gly Ser
            740                 745
```

<210> 191
<211> 758
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 191
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1   5   10   15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35   40   45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65   70   75   80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100   105   110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115   120   125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130   135   140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145   150   155   160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165   170   175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180   185   190

```
Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro
                245                 250                 255

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
            260                 265                 270

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
        275                 280                 285

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
    290                 295                 300

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Asn His Arg Asn
305                 310                 315                 320

Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp Tyr Met Asn Met Thr
                325                 330                 335

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
            340                 345                 350

Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val Lys Phe Ser Arg Ser
        355                 360                 365

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
    370                 375                 380

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
```

385 390 395 400

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
405 410 415

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
420 425 430

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
435 440 445

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
450 455 460

Leu His Met Gln Ala Leu Pro Pro Arg Arg Ala Lys Arg Ser Gly Ser
465 470 475 480

Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn
485 490 495

Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu
500 505 510

Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile
515 520 525

Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His
530 535 540

Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val
545 550 555 560

Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln
565 570 575

Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu
580 585 590

```
Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn
        595                 600                 605

Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu
    610                 615                 620

Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys
625                 630                 635                 640

Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys
                645                 650                 655

Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln
            660                 665                 670

Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr
        675                 680                 685

Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro
    690                 695                 700

Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
705                 710                 715                 720

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ile Thr Leu Ile Ile
                725                 730                 735

Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ala Leu Leu
            740                 745                 750

Ile Trp Gly Gly Gly Ser
        755
```

<210> 192
<211> 747
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 192
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
100 105 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
115 120 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
130 135 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145 150 155 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
165 170 175

```
Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
                245                 250                 255

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
            260                 265                 270

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
        275                 280                 285

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
    290                 295                 300

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
305                 310                 315                 320

Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
                325                 330                 335

Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
            340                 345                 350

Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
        355                 360                 365
```

```
Tyr Lys Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
    370                 375                 380

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
385                 390                 395                 400

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
                405                 410                 415

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
            420                 425                 430

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
        435                 440                 445

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
    450                 455                 460

Leu Pro Pro Arg Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly
465                 470                 475                 480

Asp Val Glu Ser Asn Pro Gly Pro Met Arg Leu Pro Ala Gln Leu Leu
                485                 490                 495

Gly Leu Leu Met Leu Trp Val Pro Gly Ser Ser Gly Arg Lys Val Cys
            500                 505                 510

Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala
        515                 520                 525

Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu
    530                 535                 540

His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr Pro
545                 550                 555                 560
```

```
Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu Ile
                565                 570                 575

Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu
            580                 585                 590

His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg Thr Lys Gln His
        595                 600                 605

Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile Thr Ser Leu Gly
    610                 615                 620

Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val Ile Ile Ser Gly
625                 630                 635                 640

Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe
                645                 650                 655

Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn
            660                 665                 670

Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu Cys Ser Pro Glu
        675                 680                 685

Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser Gly Gly Gly Gly
    690                 695                 700

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
705                 710                 715                 720

Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly Thr Ile
                725                 730                 735

Leu Leu Ala Leu Leu Ile Trp Gly Gly Gly Ser
            740                 745
```

<210> 193

<211> 666
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 193
Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
1 5 10 15

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
20 25 30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
100 105 110

Thr Ser Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln Ile Thr Cys Pro
130 135 140

Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val Lys Ser Tyr Ser
145 150 155 160

```
Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly Phe Lys Arg Lys
                165                 170                 175

Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn Lys Ala Thr Asn
            180                 185                 190

Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile Arg Asp Pro Ala
        195                 200                 205

Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val Thr Thr Ala Gly
    210                 215                 220

Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly Lys Glu Pro Ala
225                 230                 235                 240

Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr Thr Ala Ala Ile
                245                 250                 255

Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro Ser Thr Gly Thr
            260                 265                 270

Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr Pro Ser Gln Thr
        275                 280                 285

Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser His Gln Pro Pro
    290                 295                 300

Gly Val Tyr Pro Gln Gly His Ser Asp Thr Thr Val Ala Ile Ser Thr
305                 310                 315                 320

Ser Thr Val Leu Leu Cys Gly Leu Ser Ala Val Ser Leu Leu Ala Cys
                325                 330                 335

Tyr Leu Lys Ser Arg Gln Thr Pro Pro Leu Ala Ser Val Glu Met Glu
            340                 345                 350

Ala Met Glu Ala Leu Pro Val Thr Trp Gly Thr Ser Ser Arg Asp Glu
```

```
        355                 360                 365

Asp Leu Glu Asn Cys Ser His His Leu Arg Ala Lys Arg Gly Ser Gly
    370                 375                 380

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
385                 390                 395                 400

Gly Pro Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp
                405                 410                 415

Val Pro Gly Ser Ser Gly Arg Lys Val Cys Asn Gly Ile Gly Ile Gly
            420                 425                 430

Glu Phe Lys Asp Ser Leu Ser Ile Asn Ala Thr Asn Ile Lys His Phe
        435                 440                 445

Lys Asn Cys Thr Ser Ile Ser Gly Asp Leu His Ile Leu Pro Val Ala
    450                 455                 460

Phe Arg Gly Asp Ser Phe Thr His Thr Pro Pro Leu Asp Pro Gln Glu
465                 470                 475                 480

Leu Asp Ile Leu Lys Thr Val Lys Glu Ile Thr Gly Phe Leu Leu Ile
                485                 490                 495

Gln Ala Trp Pro Glu Asn Arg Thr Asp Leu His Ala Phe Glu Asn Leu
            500                 505                 510

Glu Ile Ile Arg Gly Arg Thr Lys Gln His Gly Gln Phe Ser Leu Ala
        515                 520                 525

Val Val Ser Leu Asn Ile Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu
    530                 535                 540

Ile Ser Asp Gly Asp Val Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr
545                 550                 555                 560
```

Ala Asn Thr Ile Asn Trp Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys
565 570 575

Thr Lys Ile Ile Ser Asn Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly
580 585 590

Gln Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu
595 600 605

Pro Arg Asp Cys Val Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
610 615 620

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val
625 630 635 640

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
645 650 655

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser
660 665

<210> 194
<211> 971
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 194
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile

```
        35                  40                  45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240
```

```
Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
    370                 375                 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430
```

```
Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val
465                 470                 475                 480

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
                485                 490                 495

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser
            500                 505                 510

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
        515                 520                 525

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
    530                 535                 540

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
545                 550                 555                 560

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
                565                 570                 575

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
            580                 585                 590

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
        595                 600                 605

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
    610                 615                 620
```

```
Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
625                 630                 635                 640

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala
                645                 650                 655

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
            660                 665                 670

Gly Pro Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala
        675                 680                 685

Glu Pro Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu
    690                 695                 700

Phe Arg Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met
705                 710                 715                 720

Arg Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe
                725                 730                 735

His Ile Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala
            740                 745                 750

Pro Ile Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr
        755                 760                 765

Ile Ile Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys
    770                 775                 780

Cys Leu Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala
785                 790                 795                 800

Ala Ile Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys
                805                 810                 815

Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His
```

```
            820                 825                 830

Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu
        835                 840                 845

Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe
    850                 855                 860

Leu Gly Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu
865                 870                 875                 880

Val Ile Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg
                885                 890                 895

Pro Lys Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln
            900                 905                 910

Thr Ile Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser
        915                 920                 925

Gln Pro Lys Asn Glu Glu Asp Ile Glu Ile Ile Pro Ile Gln Glu Glu
    930                 935                 940

Glu Glu Glu Glu Thr Glu Thr Asn Phe Pro Glu Pro Pro Gln Asp Gln
945                 950                 955                 960

Glu Ser Ser Pro Ile Glu Asn Asp Ser Ser Pro
                965                 970
```

<210> 195
<211> 937
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 195

```
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1               5                  10                  15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35                  40                  45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100                 105                 110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115                 120                 125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130                 135                 140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145                 150                 155                 160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165                 170                 175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180                 185                 190

Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
```

```
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
    370                 375                 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
385                 390                 395                 400
```

```
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val
465                 470                 475                 480

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
                485                 490                 495

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser
            500                 505                 510

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
        515                 520                 525

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
    530                 535                 540

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
545                 550                 555                 560

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
                565                 570                 575

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
            580                 585                 590
```

```
Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
        595                 600                 605

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
    610                 615                 620

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
625                 630                 635                 640

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala
                645                 650                 655

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
            660                 665                 670

Gly Pro Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala
        675                 680                 685

Glu Pro Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu
    690                 695                 700

Phe Arg Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met
705                 710                 715                 720

Arg Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe
                725                 730                 735

His Ile Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala
            740                 745                 750

Pro Ile Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr
        755                 760                 765

Ile Ile Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys
    770                 775                 780
```

```
Cys Leu Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala
785                 790                 795                 800


Ala Ile Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys
                805                 810                 815


Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His
            820                 825                 830


Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu
        835                 840                 845


Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe
    850                 855                 860


Leu Gly Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu
865                 870                 875                 880


Val Ile Ala Gly Ile Val Glu Asn Glu Trp Lys Arg Thr Cys Ser Arg
                885                 890                 895


Pro Lys Ser Asn Ile Val Leu Leu Ser Ala Glu Glu Lys Lys Glu Gln
            900                 905                 910


Thr Ile Glu Ile Lys Glu Glu Val Val Gly Leu Thr Glu Thr Ser Ser
        915                 920                 925


Gln Pro Lys Asn Glu Glu Asp Ile Glu
    930                 935


<210> 196
<211> 888
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide
```

<400> 196
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1   5   10   15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
        35   40   45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65   70   75   80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly
            100   105   110

Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys
        115   120   125

Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser
    130   135   140

Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser
145   150   155   160

Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile
                165   170   175

Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu
            180   185   190

```
Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn
        195                 200                 205

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr
    210                 215                 220

Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
225                 230                 235                 240

Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys
                245                 250                 255

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
            260                 265                 270

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
        275                 280                 285

Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp
    290                 295                 300

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
305                 310                 315                 320

Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
                325                 330                 335

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
            340                 345                 350

Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
        355                 360                 365

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu
    370                 375                 380

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
```

```
385                 390                 395                 400

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
                405                 410                 415

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
            420                 425                 430

Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn
        435                 440                 445

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
    450                 455                 460

Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val
465                 470                 475                 480

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
                485                 490                 495

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser
            500                 505                 510

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
        515                 520                 525

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg
    530                 535                 540

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
545                 550                 555                 560

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
                565                 570                 575

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
            580                 585                 590
```

```
Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
        595                 600                 605

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
    610                 615                 620

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
625                 630                 635                 640

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Ala
                645                 650                 655

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
            660                 665                 670

Gly Pro Met Thr Thr Pro Arg Asn Ser Val Asn Gly Thr Phe Pro Ala
        675                 680                 685

Glu Pro Met Lys Gly Pro Ile Ala Met Gln Ser Gly Pro Lys Pro Leu
    690                 695                 700

Phe Arg Arg Met Ser Ser Leu Val Gly Pro Thr Gln Ser Phe Phe Met
705                 710                 715                 720

Arg Glu Ser Lys Thr Leu Gly Ala Val Gln Ile Met Asn Gly Leu Phe
                725                 730                 735

His Ile Ala Leu Gly Gly Leu Leu Met Ile Pro Ala Gly Ile Tyr Ala
            740                 745                 750

Pro Ile Cys Val Thr Val Trp Tyr Pro Leu Trp Gly Gly Ile Met Tyr
        755                 760                 765

Ile Ile Ser Gly Ser Leu Leu Ala Ala Thr Glu Lys Asn Ser Arg Lys
    770                 775                 780
```

Cys Leu Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala
785 790 795 800

Ala Ile Ser Gly Met Ile Leu Ser Ile Met Asp Ile Leu Asn Ile Lys
805 810 815

Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala His
820 825 830

Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu
835 840 845

Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser Leu Phe
850 855 860

Leu Gly Ile Leu Ser Val Met Leu Ile Phe Ala Phe Phe Gln Glu Leu
865 870 875 880

Val Ile Ala Gly Ile Val Glu Asn
885

<210> 197
<211> 848
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 197
Met Lys Arg Phe Leu Phe Leu Leu Leu Thr Ile Ser Leu Leu Val Met
1 5 10 15

Val Gln Ile Gln Thr Gly Leu Ser Gly Gln Asn Asp Thr Ser Gln Thr
20 25 30

Ser Ser Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly
35 40 45

```
Glu Gly Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser
    50                  55                  60

Pro Ser Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly
65                  70                  75                  80

Ser Thr Lys Gly Gly Gln Asn Asp Thr Ser Gln Thr Ser Ser Pro Ser
                85                  90                  95

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
            100                 105                 110

Lys Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Lys Pro Phe Trp
        115                 120                 125

Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val
    130                 135                 140

Thr Val Ala Phe Ile Ile Phe Trp Val Ala Thr Asn Phe Ser Leu Leu
145                 150                 155                 160

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro
                165                 170                 175

Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg
            180                 185                 190

Pro Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu
        195                 200                 205

Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys
    210                 215                 220

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu
225                 230                 235                 240
```

```
Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
                245                 250                 255

Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
            260                 265                 270

Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
        275                 280                 285

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser
    290                 295                 300

Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val
305                 310                 315                 320

Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu
                325                 330                 335

Ser Val Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val
            340                 345                 350

Ser Trp Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val
        355                 360                 365

Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg
    370                 375                 380

Leu Thr Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met
385                 390                 395                 400

Asn Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His
                405                 410                 415

Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
            420                 425                 430
```

```
Ser Val Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
        435                 440                 445

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
    450                 455                 460

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
465                 470                 475                 480

Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
                485                 490                 495

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
            500                 505                 510

Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
        515                 520                 525

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
    530                 535                 540

Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
545                 550                 555                 560

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
                565                 570                 575

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
            580                 585                 590

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
        595                 600                 605

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
    610                 615                 620

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
```

625 630 635 640

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
645 650 655

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu
660 665 670

Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val
675 680 685

Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His
690 695 700

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys
705 710 715 720

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
725 730 735

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
740 745 750

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
755 760 765

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
770 775 780

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
785 790 795 800

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
805 810 815

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
820 825 830

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
        835   840   845

<210> 198
<211> 910
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 198
Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro
1   5   10   15

Gly Ser Ser Gly Arg Cys Ala Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr
            20   25   30

Gly Arg Cys Glu Ala Cys Arg Val Cys Glu Ala Gly Ser Gly Leu Val
        35   40   45

Phe Ser Cys Gln Asp Lys Gln Asn Thr Val Cys Glu Glu Cys Pro Asp
    50   55   60

Gly Thr Tyr Ser Asp Glu Ala Asn His Val Asp Pro Cys Leu Pro Cys
65   70   75   80

Thr Val Cys Glu Asp Thr Glu Arg Gln Leu Arg Glu Cys Thr Arg Trp
                85   90   95

Ala Asp Ala Glu Cys Glu Glu Ile Pro Gly Arg Trp Ile Thr Arg Ser
            100   105   110

Thr Pro Pro Glu Gly Ser Asp Ser Thr Ala Pro Ser Thr Gln Glu Pro
        115   120   125

Glu Ala Pro Pro Glu Gln Asp Leu Ile Ala Ser Thr Val Ala Gly Val

```
    130                 135                 140

Val Thr Thr Val Met Gly Ser Ser Gln Pro Val Val Thr Arg Gly Thr
145                 150                 155                 160

Thr Asp Asn Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                165                 170                 175

Gly Ser Gly Gly Gly Gly Ser Phe Trp Val Leu Val Val Val Gly Gly
            180                 185                 190

Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
        195                 200                 205

Trp Val Arg Ser Lys Arg Ser Ala Thr Asn Phe Ser Leu Leu Lys Gln
    210                 215                 220

Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
225                 230                 235                 240

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asp
                245                 250                 255

Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp
            260                 265                 270

Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Lys Tyr Leu
        275                 280                 285

Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr
    290                 295                 300

His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
305                 310                 315                 320

Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu
                325                 330                 335
```

```
Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr Thr
            340                 345                 350

Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Ser Thr Ser Gly Ser
        355                 360                 365

Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr Lys Gly Glu Val Lys Leu
    370                 375                 380

Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val
385                 390                 395                 400

Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp
                405                 410                 415

Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp
            420                 425                 430

Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr
        435                 440                 445

Ile Ile Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser
    450                 455                 460

Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr
465                 470                 475                 480

Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
                485                 490                 495

Thr Val Ser Ser Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
            500                 505                 510

Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
        515                 520                 525
```

```
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
    530                 535                 540

Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
545                 550                 555                 560

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
                565                 570                 575

Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
            580                 585                 590

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
        595                 600                 605

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
    610                 615                 620

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
625                 630                 635                 640

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
                645                 650                 655

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
            660                 665                 670

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
        675                 680                 685

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
    690                 695                 700

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
705                 710                 715                 720
```

```
Lys Ser Leu Ser Leu Ser Leu Gly Lys Met Phe Trp Val Leu Val Val
                725                 730                 735

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
            740                 745                 750

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Gly Gly His Ser Asp
        755                 760                 765

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
    770                 775                 780

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Arg Val
785                 790                 795                 800

Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn
                805                 810                 815

Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val
            820                 825                 830

Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg
        835                 840                 845

Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys
    850                 855                 860

Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg
865                 870                 875                 880

Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys
                885                 890                 895

Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            900                 905                 910
```

<210> 199

<211> 513
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 199
cgcaaagtgt gtaacggaat aggtattggt gaatttaaag actcactctc cataaatgct 60

acgaatatta aacacttcaa aaactgcacc tccatcagtg gcgatctcca catcctgccg 120

gtggcattta ggggtgactc cttcacacat actcctcctc tggatccaca ggaactggat 180

attctgaaaa ccgtaaagga aatcacaggg tttttgctga ttcaggcttg gcctgaaaac 240

aggacggacc tccatgcctt tgagaaccta gaaatcatac gcggcaggac caagcaacat 300

ggtcagtttt ctcttgcagt cgtcagcctg aacataacat ccttgggatt acgctccctc 360

aaggagataa gtgatggaga tgtgataatt tcaggaaaca aaaatttgtg ctatgcaaat 420

acaataaact ggaaaaaact gtttgggacc tccggtcaga aaaccaaaat tataagcaac 480

agaggtgaaa acagctgcaa ggccacaggc cag 513

<210> 200
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 200
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

```
Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
    50                  55                  60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65                  70                  75                  80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
                85                  90                  95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100                 105                 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln
                165                 170
```

<210> 201
<211> 423
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 201
gtctgccatg ccttgtgctc ccccgagggc tgctggggcc cggagcccag ggactgcgtc 60

tcttgccgga atgtcagccg aggcagggaa tgcgtggaca agtgcaacct tctggagggt 120

gagccaaggg agtttgtgga gaactctgag tgcatacagt gccacccaga gtgcctgcct 180

caggccatga acatcacctg cacaggacgg ggaccagaca actgtatcca gtgtgcccac 240

tacattgacg gcccccactg cgtcaagacc tgcccggcag gagtcatggg agaaaacaac 300

accctggtct ggaagtacgc agacgccggc catgtgtgcc acctgtgcca tccaaactgc 360

acctacggat gcactgggcc aggtcttgaa ggctgtccaa cgaatgggcc taagatcccg 420

tcc 423

<210> 202
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 202
Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1 5 10 15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
20 25 30

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
35 40 45

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
50 55 60

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
65 70 75 80

Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met
85 90 95

Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val
100 105 110

Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly
        115   120   125

Leu Glu Gly Cys Pro Thr Asn Gly Pro Lys Ile Pro Ser
    130   135   140

<210> 203
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 203
Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1   5   10   15

Arg Asp Cys Val Ser
            20

<210> 204
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 204
Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1   5   10   15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
            20   25   30

Asp Lys

<210> 205

<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 205
Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1 5 10 15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
20 25 30

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
35 40 45

Ser Glu Cys Ile Gln
50

<210> 206
<211> 77
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 206
Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1 5 10 15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
20 25 30

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
35 40 45

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
50 55 60

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln
65 70 75

<210> 207
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 207
Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1 5 10 15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
20 25 30

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
35 40 45

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
50 55 60

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
65 70 75 80

Tyr Ile Asp Gly Pro His Cys Val Lys Thr
85 90

<210> 208
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 208
Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1   5   10   15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
            20   25   30

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
        35   40   45

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
    50   55   60

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
65   70   75   80

Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met
                85   90   95

Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val
            100   105   110

Cys His Leu
        115

<210> 209
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 209
Val Cys His Ala Leu Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro
1   5   10   15

Arg Asp Cys Val Ser Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val
            20   25   30

Asp Lys Cys Asn Leu Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn
        35   40   45

Ser Glu Cys Ile Gln Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn
    50   55   60

Ile Thr Cys Thr Gly Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His
65   70   75   80

Tyr Ile Asp Gly Pro His Cys Val Lys Thr Cys Pro Ala Gly Val Met
                85   90   95

Gly Glu Asn Asn Thr Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val
            100   105   110

Cys His Leu Cys His Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly
        115   120   125

Leu Glu Gly Cys Pro
    130

<210> 210
<211> 312
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 210
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1   5   10   15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
            20   25   30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe

```
        35                  40                  45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
    50                  55                  60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65                  70                  75                  80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
                85                  90                  95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100                 105                 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
    210                 215                 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225                 230                 235                 240
```

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
245 250 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
260 265 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
275 280 285

Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
290 295 300

Thr Asn Gly Pro Lys Ile Pro Ser
305 310

<210> 211
<211> 192
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 211
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn

65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

<210> 212
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 212
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

```
Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
        35                  40                  45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
    50                  55                  60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65                  70                  75                  80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
                85                  90                  95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100                 105                 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys
        195                 200                 205
```

<210> 213
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 213
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
165 170 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
180 185 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
195 200 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

<210> 214
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 214
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

```
Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125


Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140


Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160


Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175


Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190


Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205


Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
    210                 215                 220


Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225                 230                 235                 240


Arg Gly Pro Asp Asn Cys Ile Gln
                245


<210> 215
<211> 261
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 215
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1               5                   10                  15
```

```
Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
            20                  25                  30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
        35                  40                  45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
    50                  55                  60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65                  70                  75                  80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
                85                  90                  95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100                 105                 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205
```

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
210 215 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225 230 235 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
245 250 255

His Cys Val Lys Thr
260

<210> 216
<211> 286
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 216
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

```
Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
            100                 105                 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
        115                 120                 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
    130                 135                 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145                 150                 155                 160

Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175

Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190

Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205

Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
    210                 215                 220

Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225                 230                 235                 240

Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
                245                 250                 255

His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
            260                 265                 270

Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu
        275                 280                 285
```

<210> 217
<211> 304
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 217
Arg Lys Val Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu
1 5 10 15

Ser Ile Asn Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile
20 25 30

Ser Gly Asp Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe
35 40 45

Thr His Thr Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr
50 55 60

Val Lys Glu Ile Thr Gly Phe Leu Leu Ile Gln Ala Trp Pro Glu Asn
65 70 75 80

Arg Thr Asp Leu His Ala Phe Glu Asn Leu Glu Ile Ile Arg Gly Arg
85 90 95

Thr Lys Gln His Gly Gln Phe Ser Leu Ala Val Val Ser Leu Asn Ile
100 105 110

Thr Ser Leu Gly Leu Arg Ser Leu Lys Glu Ile Ser Asp Gly Asp Val
115 120 125

Ile Ile Ser Gly Asn Lys Asn Leu Cys Tyr Ala Asn Thr Ile Asn Trp
130 135 140

Lys Lys Leu Phe Gly Thr Ser Gly Gln Lys Thr Lys Ile Ile Ser Asn
145 150 155 160

```
Arg Gly Glu Asn Ser Cys Lys Ala Thr Gly Gln Val Cys His Ala Leu
                165                 170                 175


Cys Ser Pro Glu Gly Cys Trp Gly Pro Glu Pro Arg Asp Cys Val Ser
            180                 185                 190


Cys Arg Asn Val Ser Arg Gly Arg Glu Cys Val Asp Lys Cys Asn Leu
        195                 200                 205


Leu Glu Gly Glu Pro Arg Glu Phe Val Glu Asn Ser Glu Cys Ile Gln
    210                 215                 220


Cys His Pro Glu Cys Leu Pro Gln Ala Met Asn Ile Thr Cys Thr Gly
225                 230                 235                 240


Arg Gly Pro Asp Asn Cys Ile Gln Cys Ala His Tyr Ile Asp Gly Pro
                245                 250                 255


His Cys Val Lys Thr Cys Pro Ala Gly Val Met Gly Glu Asn Asn Thr
            260                 265                 270


Leu Val Trp Lys Tyr Ala Asp Ala Gly His Val Cys His Leu Cys His
        275                 280                 285


Pro Asn Cys Thr Tyr Gly Cys Thr Gly Pro Gly Leu Glu Gly Cys Pro
    290                 295                 300


<210> 218
<211> 47
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 218
Lys Ile Ser His Phe Leu Lys Met Glu Ser Leu Asn Phe Ile Arg Ala
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1 5 10 15

His Thr Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser
20 25 30

Glu Lys Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser
35 40 45

<210> 219
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 219
Pro Tyr Ile Asn Ile Tyr Asn Cys Glu Pro Ala Asn Pro Ser Glu Lys
1 5 10 15

Asn Ser Pro Ser Thr Gln Tyr Cys Tyr Ser Ile Gln Ser
20 25

<210> 220
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 220
Cys Glu Pro Ala Asn Pro Ser Glu Lys Asn Ser Pro Ser Thr Gln Tyr
1 5 10 15

Cys

<210> 221
<211> 5

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 221
Gly Gly Gly Gly Ser
1 5

<210> 222
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MISC_FEATURE
<222> (1)..(25)
<223> This sequence may encompass 1-5 "Gly Gly Gly Gly Ser"
repeating units

<400> 222
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 223
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 223
Ser Gly Gly Gly Gly Ser
1 5

<210> 224
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 224
Gly Gly Gly Ser
1

<210> 225
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 225
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro
1 5 10

<210> 226
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 226
Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Ser Leu Gln
20 25

<210> 227

<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 227
Arg Ala Lys Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys
1 5 10 15

Gly Asp Val Glu Glu Asn Pro Gly Pro
20 25

<210> 228
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 228
Arg Ala Lys Arg Ser Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
1 5 10 15

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
20 25

<210> 229
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Val or Ile

<220>
<221> MOD_RES
<222> (4)..(4)
<223> Any amino acid

<400> 229
Asp Xaa Glu Xaa Asn Pro Gly Pro
1   5

<210> 230
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 230
Arg Ala Lys Arg
1

<210> 231
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 231
agagctaaga gg   12

<210> 232
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 232
cgtgcaaagc gt   12

<210> 233
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 233
Arg Ala Lys Arg Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu
1 5 10 15

Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 234
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 234
agagccaaga gggcaccggt gaaacagact ttgaattttg accttctgaa gttggcagga 60

gacgttgagt ccaaccctgg gccc 84

<210> 235
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 235
Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
            20

<210> 236
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 236
ggaagcggag ctactaactt cagcctgctg aagcaggctg gagacgtgga ggagaaccct   60

ggacct   66

<210> 237
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

<400> 237
Arg Ala Lys Arg Ala Pro Val Lys Gln Gly Ser Gly Ala Thr Asn Phe
1   5   10   15

Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro
            20   25   30

<210> 238
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide

<400> 238
cgtgcaaagc gtgcaccggt gaaacaggga agcggagcta ctaacttcag cctgctgaag   60

caggctggag acgtggagga gaaccctgga cct 93

<210> 239
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (5)..(5)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (7)..(7)
<223> Any amino acid

<220>
<221> MOD_RES
<222> (9)..(9)
<223> Any amino acid

<220>
<221> MISC_FEATURE
<222> (1)..(10)
<223> This sequence may encompass 2-5 "Xaa Pro" repeating units

<400> 239
Xaa Pro Xaa Pro Xaa Pro Xaa Pro Xaa Pro
1 5 10

<210> 240
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MISC_FEATURE
<222> (2)..(26)
<223> This region may encompass 2-5 "Glu Ala Ala Ala Lys"
repeating units

<400> 240
Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
1 5 10 15

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
20 25